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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : G01N 33/50, C12Q 1/48, 1/25		A3	(11) International Publication Number: WO 98/45704 (43) International Publication Date: 15 October 1998 (15.10.98)
(21) International Application Number: PCT/DK98/00145 (22) International Filing Date: 7 April 1998 (07.04.98) (30) Priority Data: 0392/97 7 April 1997 (07.04.97) DK		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(71) Applicant (<i>for all designated States except US</i>): NOVO NORDISK A/S [DK/DK]; Novo Allé, DK-2880 Bagsværd (DK). (72) Inventors; and (75) Inventors/Applicants (<i>for US only</i>): THASTRUP, Ole [DK/DK]; Birkevej 37, DK-3460 Birkerød (DK). PETERSEN BJØRN, Sara [DK/DK]; Klampenborgvej 102, DK-2800 Lyngby (DK). TULLIN, Søren [DK/DK]; Karl Gjellerups Alle 18, DK-2860 Søborg (DK). KASPER, Almholt [DK/DK]; Eigtsgade 32, 4. tv, DK-2300 København S (DK). SCUDDER, Kurt [US/DK]; Lavendelhaven 70, DK-2830 Virum (DK). (74) Common Representative: NOVO NORDISK A/S; attn. Lars Kellberg, Novo Allé, DK-2880 Bagsværd (DK).		Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 22 April 1999 (22.04.99)	
(54) Title: A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE			
(57) Abstract			
<p>Cells are genetically modified to expresss a luminophore, e.g., a modified (F64L, S65T, Y66H) Green Fluorescent Protein (GFP, EGFP) coupled to a component of an intracellular signalling pathway such as a transcription factor, a cGMP- or cAMP-dependent protein kinase, a cyclin-, calmodulin- or phospholipid-dependent or mitogen-activated serine/threonin protein kinase, a tyrosine protein kinase, or a protein phosphatase (e.g. PKA, PKC, Erk, Smad, VASP, actin, p38, Jnk1, PKG, IkappaB, CDK2, Grk5, Zap70, p85, protein-tyrosine phosphatase 1C, Stat5, NFAT, NFkappaB, RhoA, PKB). An influence modulates the intracellular signalling pathway in such a way that the luminophore is being redistributed or translocated with the component in living cells in a manner experimentally determined to be correlated to the degree of the influence. Measurement of redistribution is performed by recording of light intensity, fluorescence lifetime, polarization, wavelength shift, resonance energy transfer, or other properties by an apparatus consisting of e.g. a fluorescence microscope and a CCD camera. Data stored as digital images are processed to numbers representing the degree of redistribution. The method can be used as a screening program for identifying a compound that modulates a component and is capable of treating a disease related to the function of the component.</p>			

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 98/00145

A. CLASSIFICATION OF SUBJECT MATTER			
IPC 6	G01N33/50	C12Q1/48	C12Q1/25

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 G01N C12Q C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 11094 A (NOVONORDISK AS ;THASTRUP OLE (DK); TULLIN SOEREN (DK); POULSEN LAR) 27 March 1997	1-27, 30-40, 44-60, 64-82,88
Y	see the whole document see claims	28,29, 41,61-63
X	---	1-27, 30-40, 42-60, 64-84, 87,88
Y	WO 91 01305 A (UNIV WALES MEDICINE) 7 February 1991	28,29, 41,61-63
Y	see page 4, line 15 - line 20 see claims	28,29, 41,61-63
	see examples 1-10	---
		-/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

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- X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents such combination being obvious to a person skilled in the art
- Z document member of the same patent family

Date of the actual completion of the international search

19 January 1999

Date of mailing of the International search report

25.02.1999

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 98/00145

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 07463 A (UNIV COLUMBIA ;WOODS HOLE OCEANOGRAPHIC INST (US); CHALFIE MARTIN) 16 March 1995 cited in the application	1-27, 30-40, 42-60, 64-84, 87,88
Y	see claim 26 see the whole document	28,29, 41,61-63
Y	---	
Y	WO 96 23898 A (NOVONORDISK AS ;THASTRUP OLE (DK); TULLIN SOEREN (DK); POULSEN LAR) 8 August 1996	28,29, 41,61-63
X	see the whole document	
X	see page 8-17	42,43, 46,47
X	---	
X	WO 96 03649 A (UNIV NORTH CAROLINA) 8 February 1996 see page 49; example 6.10	45
P,X	WO 97 20931 A (US HEALTH ;HTUN HAN (US); HAGER GORDON L (US)) 12 June 1997 see claims 41-58	40,44
P,X	---	
P,X	WO 97 30074 A (CYTOGEN CORP ;UNIV NORTH CAROLINA (US)) 21 August 1997 see page 57	44
P,X	---	
E	WO 98 02571 A (TSIEN ROGER Y ;CUBITT ANDREW B (US); UNIV CALIFORNIA (US)) 22 January 1998 see claims	1-27, 30-40, 42-50, 52-54, 57-60, 64-82,88
E	see claims	
E	---	
E	WO 98 30715 A (ISACOFF EHUD Y ;SIEGAL MICAH S (US); UNIV CALIFORNIA (US); CALIFOR) 16 July 1998 see the whole document	1-84,87, 88
E	---	
	-/-	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 98/00145

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	SAKAI, N. ET AL.: "Direct visualization of the translocation of the gamma subspecies of protein kinase c in living cells using fusion proteins with green fluorescent protein." THE JOURNAL OF CELL BIOLOGY, vol. 139, no. 6, 15 December 1997, pages 1465-1476, XP002078902 see the whole document	1-43,46, 47,49, 53-57, 59-82,88
O,X	& Direct visualization of the translocation of the gamma subspecies of protein kinase c in living cells using fusion proteins with green fluorescent protein. Meeting held at 22-23.03.97 cited in the application see abstract ---	
X	SCHMIDT, D.J. ET AL.: "Dynamic analysis of alpha-PKC-GFP chimera translocation events in smooth muscle with ultra-high speed 3D fluorescence microscopy" FASEB JOURNAL, vol. 11, no. 3, 28 February 1997, page A505 XP002077257 cited in the application see abstract ---	1-43,46, 47,49, 53-57, 59-82,88
X	GERISCH, GUENTHER ET AL: "Chemoattractant-controlled accumulation of coronin at the leading edge of Dictyostelium cells monitored using a green fluorescent protein-coronin fusion protein" CURR. BIOL. (1995), 5(11), 1280-5 CODEN: CUBLE2;ISSN: 0960-9822, XP002089510 see abstract p 1281, right col, second full , last sentence ---	1,40,43, 45
X	SIDOROVA, JULIA M. ET AL: "Cell cycle-regulated phosphorylation of Swi6 controls its nuclear localization" MOL. BIOL. CELL (1995), 6(12), 1641-58 CODEN: MBCEEV;ISSN: 1059-1524, XP002089512 see the whole document ---	40,43,44
X	HAN HTUN ET AL: "VISUALIZATION OF GLUCOCORTICOID RECEPTOR TRANSLOCATION AND INTRANUCLEAR ORGANIZATION IN LIVING CELLS WITH A GREEN FLUORESCENT PROTEIN CHIMERA" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 93, no. 10, May 1996, pages 4845-4850, XP002029560 see the whole document ---	1-40,44, 64-72

INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 98/00145

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CAREY K L ET AL: "EVIDENCE USING A GREEN FLUORESCENT PROTEIN-GLUCOCORTICOID RECEPTOR CHIMERA THAT THE RAN/TC4 GTPASE MEDIATES AN ESSENTIAL FUNCTION INDEPENDENT OF NUCLEAR PROTEIN IMPORT" THE JOURNAL OF CELL BIOLOGY, vol. 133, no. 5, June 1996, pages 985-996, XP000670316 cited in the application see the whole document ----	1-40, 44, 64-72
X	OGAWA H ET AL: "LOCALIZATION, TRAFFICKING, AND TEMPERATURE-DEPENDENCE OF THE AEQUOREA GREEN FLUORESCENT PROTEIN IN CULTURES VERTEBRATE CELLS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 92, no. 25, 5 December 1995, pages 11899-11903, XP002029556 see the whole document	1-40, 44, 64-72
X	WESTPHAL, MONIKA ET AL: "Microfilament dynamics during cell movement and chemotaxis monitored using a GFP - actin fusion protein" CURR. BIOL. (1997), 7(3), 176-183 CODEN: CUBLE2;ISSN: 0960-9822, XP002090291 see page 181, left-hand column, line 1	1, 40, 43, 45
X	TODA, TAKASHI ET AL: "The fission yeast sts5+ gene is required for maintenance of growth polarity and functionally interacts with protein kinase C and an osmosensing MAP kinase pathway" J. CELL SCI. (1996), 109(9), 2331-2342 CODEN: JNCSAI;ISSN: 0021-9533, XP002090292 see abstract	40, 42
A	WEBB, CHRIS D. ET AL: "Use of green fluorescent protein for visualization of cell-specific gene expression and subcellular protein localization during sporulation in <i>Bacillus subtilis</i> " J. BACTERIOL. (1995), 177(20), 5906-11 CODEN: JOBAAY;ISSN: 0021-9193, XP002089513 see the whole document	44
A	WO 94 23039 A (CANCER RES INST ROYAL MARSHALL CHRISTOPHER JOHN (GB); ASHWORTH AL) 13 October 1994 see the whole document	1-84, 87, 88

INTERNATIONAL SEARCH REPORT

Int. application No.
PCT/DK 98/00145

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 83-84 and claim 87 relate to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition (Rule 39.1(iv) PCT - Method for treatment of the human or animal body by therapy).
2. Claims Nos.: 85,86
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Claims Nos.: 85,86

The subject-matter (compounds per se) is solely characterised in claims 85 and 86 by the result to be achieved, no support of a technical character is derivable from the description for the technical formulation of the subject of the search, accordingly no scope of a search could be defined and a meaningful search is hence not possible.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Partially: 1-43, 46, 59-82 and 88; Entirely: 47, 49, 53-57

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being serine/threonine protein kinases

2. Claims: Partially: 1-41, 43, 59-82 and 88; Entirely: 48

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being tyrosine kinases

3. Claims: Partially: 1-43, 46, 59-82 and 88; Entirely: 50, 51

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being cAMP dependent protein kinases.

4. Claims: Partially: 1-43, 46, 59-82 and 88; Entirely: 52

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being cGMP dependent protein kinases

5. Claims: Partially: 1-43, 59-82 and 88; Entirely: 58

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being protein phosphatases

6. Claims: Partially: 1-41, 43, 59-82 and 88; Entirely: 44

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being transcription factors

7. Claims: Partially: 1-41, 43, 59-82 and 88; Entirely: 45

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being to proteins associated with the cytoskeletal network

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/DK 98/00145

Patent document cited in search report	Publication date	Patent family member(s)			Publication date
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(21) International Application Number: PCT/DK98/00145		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 7 April 1998 (07.04.98)			
(30) Priority Data: 0392/97 7 April 1997 (07.04.97) DK			
(71) Applicant (for all designated States except US): NOVO NORDISK A/S [DK/DK]; Novo Allé, DK-2880 Bagsvaerd (DK).		Published. <i>Without international search report and to be republished upon receipt of that report.</i>	
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(74) Common Representative: NOVO NORDISK A/S; attn. Lars Kellberg, Novo Allé, DK-2880 Bagsværd (DK).			

(54) Title: **A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE**

(57) Abstract

Cells are genetically modified to express a luminophore, e.g., a modified (F64L, S65T, Y66H) Green Fluorescent Protein (GFP, EGFP) coupled to a component of an intracellular signalling pathway such as a transcription factor, a cGMP- or cAMP-dependent protein kinase, a cyclin-, calmodulin- or phospholipid-dependent or mitogen-activated serine/threonin protein kinase, a tyrosine protein kinase, or a protein phosphatase (e.g. PKA, PKC, Erk, Smad, VASP, actin, p38, Jnk1, PKG, IkappaB, CDK2, Grk5, Zap70, p85, protein-tyrosine phosphatase 1C, Stat5, NFAT, NFkappaB, RhoA, PKB). An influence modulates the intracellular signalling pathway in such a way that the luminophore is being redistributed or translocated with the component in living cells in a manner experimentally determined to be correlated to the degree of the influence. Measurement of redistribution is performed by recording of light intensity, fluorescence lifetime, polarization, wavelength shift, resonance energy transfer, or other properties by an apparatus consisting of e.g. a fluorescence microscope and a CCD camera. Data stored as digital images are processed to numbers representing the degree of redistribution. The method can be used as a screening program for identifying a compound that modulates a component and is capable of treating a disease related to the function of the component.

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A METHOD for extracting quantitative information relating to an influence on a cellular response

FIELD OF INVENTION

5 The present invention relates to a method and tools for extracting quantitative information relating to an influence, on a cellular response, in particular an influence caused by contacting or incubating the cell with a substance influencing a cellular response, where the cellular response is manifested in redistribution of at least one component in the cell. In particular, the invention relates to a method for extracting quantitative information relating to an influence on an intracellular pathway involving redistribution of at least one component associated with the pathway. The method of the invention may be used as a very efficient procedure for testing or discovering the influence of a substance on a physiological process, for example in connection with screening for new drugs, testing of substances for toxicity, identifying drug targets for known or novel drugs. Other valuable uses of the method and technology of the
10 invention will be apparent to the skilled person on the basis of the following disclosure. In a particular embodiment of the invention, the present invention relates to a method of detecting intracellular translocation or redistribution of biologically active polypeptides, preferably an enzyme, affecting intracellular processes, and a DNA construct and a cell for use in the method.

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BACKGROUND OF THE INVENTION

Intracellular pathways are tightly regulated by a cascade of components that undergo modulation in a temporally and spatially characteristic manner. Several disease states can be attributed to altered activity of individual signalling components (i.e. protein kinases, protein phosphatases, transcription factors). These components therefore render themselves as attractive targets for therapeutic intervention.
25

Protein kinases and phosphatases are well described components of several intracellular signalling pathways. The catalytic activity of protein kinases and phosphatases are assumed to play a role in virtually all regulatable cellular processes. Although the involvement of protein kinases in cellular signalling and regulation have been subjected to extensive studies, detailed knowledge on e.g. the exact timing and spatial characteristics of signalling events is often difficult to obtain due to lack of a convenient technology.
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Novel ways of monitoring specific modulation of intracellular pathways in intact, living cells is assumed to provide new opportunities in drug discovery, functional genomics, toxicology, patient monitoring etc.

The spatial orchestration of protein kinase activity is likely to be essential for the high degree
5 of specificity of individual protein kinases. The phosphorylation mediated by protein kinases is balanced by phosphatase activity. Also within the family of phosphatases translocation has been observed, e.g. translocation of PTP2C to membrane ruffles [(Cossette et al. 1996)], and likewise is likely to be indicative of phosphatase activity.

Protein kinases often show a specific intracellular distribution before, during and after activation.
10 Monitoring the translocation processes and/or redistribution of individual protein kinases or subunits thereof is thus likely to be indicative of their functional activity. A connection between translocation and catalytic activation has been shown for protein kinases like the diacyl glycerol (DAG)-dependent protein kinase C (PKC), the cAMP-dependent protein kinase (PKA) [(DeBernardi et al. 1996)] and the mitogen-activated-protein kinase Erk-1 [(Sano et
15 al. 1995)].

Commonly used methods of detection of intracellular localisation/activity of protein kinases and phosphatases are immunoprecipitation, Western blotting and immunocytochemical detection.

Taking the family of diacyl glycerol (DAG)-dependent protein kinase Cs (PKCs) as an example,
20 it has been shown that individual PKC isoforms that are distributed among different tissues and cells have different activator requirements and undergo differential translocation in response to activation. Catalytically inactive DAG-dependent PKCs are generally distributed throughout the cytoplasm, whereas they upon activation translocate to become associated with different cellular components, e.g. plasma membrane [(Farese, 1992),(Fulop Jr. et
25 al. 1995)] nucleus [(Khalil et al. 1992)], cytoskeleton [(Blobe et al. 1996)]. The translocation phenomenon being indicative of PKC activation has been monitored using different approaches: a) immunocytochemistry where the localisation of individual isoforms can be detected after permeabilisation and fixation of the cells [(Khalil et al. 1992)]; and b) tagging all DAG-dependent PKC isoforms with a fluorescently labelled phorbol myristate acetate (PMA)
30 [(Godson et al. 1996)]; and c) chemical tagging PKC b1 with the fluorophore Cy3 [(Bastiaens & Jovin 1996)] and d) genetic tagging of PKC α [(Schrnidt et al. 1997)] and of PKC γ and PKC ϵ [(Sakai et al. 1996)]. The first method does not provide dynamic information whereas the latter methods will. Tagging PKC with fluorescently labelled phorbol myristate acetate cannot

distinguish between different DAG-dependent isoforms of PKC but will label and show movement of all isoforms. Chemical and genetic labelling of specific DAG-dependent PKCs confirmed that they in an isoform specific manner upon activation move to cell periphery or nucleus.

- 5 In an alternative method, protein kinase A activity has been measured in living cells by chemical labelling one of the kinase's subunit (Adams *et al.* 1991). The basis of the methodology is that the regulatory and catalytic subunit of purified protein kinase A is labelled with fluorescein and rhodamine, respectively. At low cAMP levels protein kinase A is assembled in a heterotetrameric form which enables fluorescence resonance energy transfer between
- 10 the two fluorescent dyes. Activation of protein kinase A leads to dissociation of the complex, thereby eliminating the energy transfer. A disadvantage of this technology is that the labelled protein kinase A has to be microinjected into the cells of interest. This highly invasive technique is cumbersome and not applicable to large scale screening of biologically active substances. A further disadvantage of this technique as compared to the presented invention is
- 15 that the labelled protein kinase A cannot be inserted into organisms/animals as a transgene. Recently it was discovered that Green Fluorescent Protein (GFP) expressed in many different cell types, including mammalian cells, became highly fluorescent [(Chalfie *et al.* 1994)]. WO95/07463 describes a cell capable of expressing GFP and a method for detecting a protein of interest in a cell based on introducing into a cell a DNA molecule having DNA se-
- 20 quence encoding the protein of interest linked to DNA sequence encoding a GFP such that the protein produced by the DNA molecule will have the protein of interest fused to the GFP, then culturing the cells in conditions permitting expression of the fused protein and detecting the location of the fluorescence in the cell, thereby localizing the protein of interest in the cell. However, examples of such fused proteins are not provided, and the use of fusion pro-
- 25 teins with GFP for detection or quantitation of translocation or redistribution of biologically active polypeptides affecting intracellular processes upon activation, such as proteins involved in signalling pathways, e.g. protein kinases or phosphatases, has not been suggested. WO 95/07463 further describes cells useful for the detection of molecules, such as hormones or heavy metals, in a biological sample, by operatively linking a regulatory ele-
- 30 ment of the gene which is affected by the molecule of interest to a GFP, the presence of the molecules will affect the regulatory element which in turn will affect the expression of the GFP. In this way the gene encoding GFP is used as a reporter gene in a cell which is constructed for monitoring the presence of a specific molecular identity.

Green Fluorescent Protein has been used in an assay for the detection of translocation of the glucocorticoid receptor (GR) [Carey, KL et al., The Journal of Cell Biology, Vol. 133, No. 5, p. 985-996 (1996)]. A GR-S65TGFP fusion has been used to study the mechanisms involved in translocation of the glucocorticoid receptor (GR) in response to the agonist dexamethasone from the cytosol, where it is present in the absence of a ligand, through the nuclear pore to the nucleus where it remains after ligand binding. The use of a GR-GFP fusion enables real-time imaging and quantitation of nuclear/cytoplasmic ratios of the fluorescence signal.

Many currently used screening programmes designed to find compounds that affect protein kinase activity are based on measurements of kinase phosphorylation of artificial or natural substrates, receptor binding and/or reporter gene expression.

DISCLOSURE OF THE INVENTION

The present invention provides an important new dimension in the investigation of cellular systems involving redistribution in that the invention provides quantification of the redistribution responses or events caused by an influence, typically contact with a chemical substance or mixture of chemical substances, but also changes in the physical environment. The quantification makes it possible to set up meaningful relationships, expressed numerically, or as curves or graphs, between the influences (or the degree of influences) on cellular systems and the redistribution response. This is highly advantageous because, as has been found, the quantification can be achieved in both a fast and reproducible manner, and - what is perhaps even more important - the systems which become quantifiable utilizing the method of the invention are systems from which enormous amounts of new information and insight can be derived.

The present screening assays have the distinct advantage over other screening assays, e.g., receptor binding assays, enzymatic assays, and reporter gene assays, in providing a system in which biologically active substances with completely novel modes of action, e.g. inhibition or promotion of redistribution/translocation of a biologically active polypeptide as a way of regulating its action rather than inhibition/activation of enzymatic activity, can be identified in a way that insures very high selectivity to the particular isoform of the biologically active polypeptide and further development of compound selectivity versus other isoforms of

the same biologically active polypeptide or other components of the same signalling pathway.

In its broadest aspect, the invention relates to a method for extracting quantitative information relating to an influence on a cellular response, the method comprising recording variation, 5 caused by the influence on a mechanically intact living cell or mechanically intact living cells, in spatially distributed light emitted from a luminophore, the luminophore being present in the cell or cells and being capable of being redistributed in a manner which is related with the degree of the influence, and/or of being modulated by a component which is capable of being redistributed in a manner which is related to the degree of the influence, the association 10 resulting in a modulation of the luminescence characteristics of the luminophore, detecting and recording the spatially distributed light from the luminophore, and processing the recorded variation in the spatially distributed light to provide quantitative information correlating the spatial distribution or change in the spatial distribution to the degree of the influence. In a preferred embodiment of the invention the luminophore, which is present in the cell or cells, 15 is capable of being redistributed by modulation of an intracellular pathway, in a manner which is related to the redistribution of at least one component of the intracellular pathway. In another preferred embodiment of the invention, the luminophore is a fluorophore.

The cells

20 In the invention the cell and/or cells are mechanically intact and alive throughout the experiment. In another embodiment of the invention, the cell or cells is/are fixed at a point in time after the application of the influence at which the response has been predetermined to be significant, and the recording is made at an arbitrary later time.

The mechanically intact living cell or cells could be selected from the group consisting of 25 fungal cell or cells, such as a yeast cell or cells; invertebrate cell or cells including insect cell or cells; and vertebrate cell or cells, such as mammalian cell or cells. This cell or these cells is/are incubated at a temperature of 30°C or above, preferably at a temperature of from 32°C to 39°C, more preferably at a temperature of from 35°C to 38°C, and most preferably at a temperature of about 37°C during the time period over which the influence is observed. In 30 one aspect of the invention the mechanically intact living cell is part of a matrix of identical or non-identical cells.

A cell used in the present invention should contain a nucleic acid construct encoding a fusion polypeptide as defined herein and be capable of expressing the sequence encoded by the construct. The cell is a eukaryotic cell selected from the group consisting of fungal cells, such as yeast cells; invertebrate cells including insect cells; vertebrate cells such as mammalian cells. The preferred cells are mammalian cells.

In another aspect of the invention the cells could be from an organism carrying in at least one of its component cells a nucleic acid sequence encoding a fusion polypeptide as defined herein and be capable of expressing said nucleic acid sequence. The organism is selected from the group consisting of unicellular and multicellular organisms, such as a mammal.

10

The luminophore

The luminophore is the component which allows the redistribution to be visualised and/or recorded by emitting light in a spatial distribution related to the degree of influence. In one embodiment of the invention, the luminophore is capable of being redistributed in a manner which is physiologically relevant to the degree of the influence. In another embodiment, the luminophore is capable of associating with a component which is capable of being redistributed in a manner which is physiologically relevant to the degree of the influence. In another embodiment, the luminophore correlation between the redistribution of the luminophore and the degree of the influence could be determined experimentally. In a preferred aspect of the invention, the luminophore is capable of being redistributed in substantially the same manner as the at least one component of an intracellular pathway. In yet another embodiment of the invention, the luminophore is capable of being quenched upon spatial association with a component which is redistributed by modulation of the pathway, the quenching being measured as a change in the intensity of the luminescence.

15 The luminophore could be a fluorophore. In a preferred embodiment of the invention, the luminophore could be a polypeptide encoded by and expressed from a nucleotide sequence harboured in the cell or cells. The luminophore could be a hybrid polypeptide comprising a fusion of at least a portion of each of two polypeptides one of which comprises a luminescent polypeptide and the other one of which comprises a biologically active polypeptide, as defined herein.

20 The luminophore could be a GFP as defined herein or could be selected from the group consisting of green fluorescent proteins having the F64L mutation as defined herein

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The luminescent polypeptide could be a GFP as defined herein or could be selected from the group consisting of green fluorescent proteins having the F64L mutation as defined herein

such as F64L-GFP, F64L-Y66H-GFP, F64L-S65T-GFP, and EGFP. The GFP could be N- or C-terminally tagged, optionally via a peptide linker, to the biologically active polypeptide or a part or a subunit thereof. The fluorescent probe could be a component of a intracellular signalling pathway. The probe is coded for by a nucleic acid construct.

- 5 The pathway of investigation in the present invention could be an intracellular signalling pathway.

The influence

- In a preferred embodiment of the invention, the influence could be contact between the mechanically intact living cell or the group of mechanically intact living cells with a chemical substance and/or incubation of the mechanically intact living cell or the group of mechanically intact living cells with a chemical substance. The influence will modulate the intracellular processes. In one aspect the modulation could be an activation of the intracellular processes. In another aspect the modulation could be an deactivation of the intracellular processes.
- 10 15 In yet another aspect, the influence could inhibit or promote the redistribution without directly affecting the metabolic activity of the component of the intracellular processes.

In one embodiment the invention is used as a basis for a screening program, where the effect of unknown influences such as a compound library, can be compared to influence of known reference compounds under standardised conditions.

20

The recording

- In addition to the intensity, there are several parameters of fluorescence or luminescence which can be modulated by the effect of the influence on the underlying cellular phenomena, and can therefore be used in the invention. Some examples are resonance energy transfer, fluorescence lifetime, polarisation, wavelength shift. Each of these methods requires a particular kind of filter in the emission light path to select the component of the light desired and reject other components. The recording of property of light could be in the form of an ordered array of values such as a CCD array or a vacuum tube device such as a vidicon tube.
- 25

In one embodiment of the invention, the spatially distributed light emitted by a luminophore could be detected by a change in the resonance energy transfer between the luminophore and another luminescent entity capable of delivering energy to the luminophore, each of

- which has been selected or engineered to become part of, bound to or associated with particular components of the intracellular pathway. In this embodiment, either the luminophore or the luminescent entity capable of delivering energy to the luminophore undergoes redistribution in response to an influence. The resonance energy transfer would be measured as a
- 5 change in the intensity of emission from the luminophore, preferably sensed by a single channel photodetector which responds only to the average intensity of the luminophore in a non-spatially resolved fashion.

In one embodiment of the invention, the recording of the spatially distributed light could be made at a single point in time after the application of the influence. In another embodiment,

10 the recording could be made at two points in time, one point being before, and the other point being after the application of the influence. The result or variation is determined from the change in fluorescence compared to the fluorescence measured prior to the influence or modulation. In another embodiment of the invention, the recording could be performed at a series of points in time, in which the application of the influence occurs at some time after

15 the first time point in the series of recordings, the recording being performed, e.g., with a predetermined time spacing of from 0.1 seconds to 1 hour, preferably from 1 to 60 seconds, more preferably from 1 to 30 seconds, in particular from 1 to 10 seconds, over a time span of from 1 second to 12 hours, such as from 10 seconds to 12 hours, e.g., from 10 seconds to one hour, such as from 60 seconds to 30 minutes or 20 minutes. The result or variation is

20 determined from the change in fluorescence over time. The result or variation could also be determined as a change in the spatial distribution of the fluorescence over time.

Apparatus

The recording of spatially distributed luminescence emitted from the luminophore is performed by an apparatus for measuring the distribution of fluorescence in the cell or cells, and thereby any change in the distribution of fluorescence in the cell or cells, which includes at a minimum the following component parts: (a) a light source, (b) a method for selecting the wavelength(s) of light from the source which will excite the fluorescence of the protein, (c) a device which can rapidly block or pass the excitation light into the rest of the system, (d) a series of optical elements for conveying the excitation light to the specimen, collecting the emitted fluorescence in a spatially resolved fashion, and forming an image from this fluorescence emission, (e) a bench or stand which holds the container of the cells being measured in a predetermined geometry with respect to the series of optical elements, (f) a detector to

record the spatially resolved fluorescence in the form of an image, (g) a computer or electronic system and associated software to acquire and store the recorded images, and to compute the degree of redistribution from the recorded images.

In a preferred embodiment of the invention the apparatus system is automated. In one embodiment the components in d and e mentioned above comprise a fluorescence microscope. In one embodiment the component in f mentioned above is a CCD camera.

In one embodiment the image is formed and recorded by an optical scanning system.

In one embodiment a liquid addition system is used to add a known or unknown compound to any or all of the cells in the cell holder at a time determined in advance. Preferably, the liquid addition system is under the control of the computer or electronic system. Such an automated system can be used for a screening program due to its ability to generate results from a larger number of test compounds than a human operator could generate using the apparatus in a manual fashion.

15 Quantitation of the influence

The recording of the variation or result with respect to light emitted from the luminophore is performed by recording the spatially distributed light as one or more digital images, and the processing of the recorded variation to reduce it to one or more numbers representative of the degree of redistribution comprises a digital image processing procedure or combination of digital image processing procedures. The quantitative information which is indicative of the degree of the cellular response to the influence or the result of the influence on the intracellular pathway is extracted from the recording or recordings according to a predetermined calibration based on responses or results, recorded in the same manner, to known degrees of a relevant specific influence. This calibration procedure is developed according to principles described below (Developing an Image-based Assay Technique). Specific descriptions of the procedures for particular assays are given in the examples.

While the stepwise procedure necessary to reduce the image or images to the value representative of the is particular to each assay, the individual steps are generally well-known methods of image processing. Some examples of the individual steps are point operations such as subtraction, ratioing, and thresholding, digital filtering methods such as smoothing, sharpening, and edge detection, spatial frequency methods such as Fourier filtering, image cross-correlation and image autocorrelation, object finding and classification (blob analysis),

and colour space manipulations for visualisation. In addition to the algorithmic procedures, heuristic methods such as neural networks may also be used.

Nucleic acid constructs

- 5 The nucleic acid constructs used in the present invention encode in their nucleic acid sequences fusion polypeptides comprising a biologically active polypeptide that is a component of an intracellular signalling pathway, or a part thereof, and a GFP, preferably an F64L mutant of GFP, N- or C-terminally fused, optionally via a peptide linker, to the biologically active polypeptide or part thereof.
- 10 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein kinase or a phosphatase.
In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a transcription factor or a part thereof which changes cellular localisation upon activation.
- 15 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein, or a part thereof, which is associated with the cytoskeletal network and which changes cellular localisation upon activation.
In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein kinase or a part thereof which changes cellular localisation upon activation.
- 20 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.
In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a tyrosine protein kinase or a part thereof capable of changing intracellular localisation upon activation.
- 25 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a phospholipid-dependent serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.
In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a cAMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation. In a preferred embodiment the biologically active polypeptide encoded by the nucleic acid construct is a PKAc-F64L-S65T-GFP fusion.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a cGMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation.

5 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a calmodulin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

10 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a mitogen-activated serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation. In preferred embodiments the biologically active polypeptide encoded by the nucleic acid constructs are an ERK1-F64L-S65T-GFP fusion or an EGFP-ERK1 fusion.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a cyclin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

15 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein phosphatase or a part thereof capable of changing cellular localisation upon activation.

In one preferred embodiment of the invention the nucleic acid constructs may be DNA constructs.

20 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct
In one embodiment the gene encoding GFP in the nucleic acid construct is derived from *Aequorea victoria*. In a preferred embodiment the gene encoding GFP in the nucleic acid construct is EGFP or a GFP variant selected from F64L-GFP, F64L-Y66H-GFP and F64L-S65T-GFP.

25 In preferred embodiments of the invention the DNA constructs which can be identified by any of the DNA sequences shown in SEQ ID NO: 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142 or are variants of these sequences capable of encoding the same fusion polypeptide or a fusion polypeptide which is biologically equivalent thereto,
30 e.g. an isoform, or a splice variant or a homologue from another species.

Screening program

- The present invention describes a method that may be used to establish a screening program for the identification of biologically active substances that directly or indirectly affects intracellular signalling pathways and because of this property are potentially useful as medicaments. Based on measurements in living cells of the redistribution of spatially resolved luminescence from luminophores which undergo a change in distribution upon activation or deactivation of an intracellular signalling pathway the result of the individual measurement of each substance being screened indicates its potential biological activity.
- In one embodiment of the invention the screening program is used for the identification of a biologically toxic substance as defined herein that exerts its toxic effect by interfering with an intracellular signalling pathway. Based on measurements in living cells of the redistribution of spatially resolved luminescence from luminophores which undergo a change in distribution upon activation or deactivation of an intracellular signalling pathway the result of the individual measurement of each substance being screened indicates its potential biologically toxic activity. In one embodiment of a screening program a compound that modulates a component of an intracellular pathway as defined herein, can be found and the therapeutic amount of the compound estimated by a method according to the method of the invention. In a preferred embodiment the present invention leads to the discovery of a new way of treating a condition or disease related to the intracellular function of a biologically active polypeptide comprising administration to a patient suffering from said condition or disease of an effective amount of a compound which has been discovered by any method according to the invention. In another preferred embodiment of the invention a method is established for identification of a new drug target or several new drug targets among the group of biologically active polypeptides which are components of intracellular signalling pathways.
- In another embodiment of the invention an individual treatment regimen is established for the selective treatment of a selected patient suffering from an ailment where the available medicaments used for treatment of the ailment are tested on a relevant primary cell or cells obtained from said patient from one or several tissues, using a method comprising transfecting the cell or cells with at least one DNA sequence encoding a fluorescent probe according to the invention, transferring the transfected cell or cells back the said patient, or culturing the cell or cells under conditions permitting the expression of said probes and exposing it to an array of the available medicaments, then comparing changes in fluorescence patterns or redistribution patterns of the fluorescent probes in the intact living cell or cells to

detect the cellular response to the specific medicaments (obtaining a cellular action profile), then selecting one or more medicament or medicaments based on the desired activity and acceptable level of side effects and administering an effective amount of these medicaments to the selected patient.

5

Back-tracking of a signal transduction pathway

The present invention describes a method that may be used to establish a screening program for back-tracking signal transduction pathways as defined herein. In one embodiment the screening program is used to establish more precisely at which level one or several 10 compounds affect a specific signal transduction pathway by successively or in parallel testing the influence of the compound or compounds on the redistribution of spatially resolved luminescence from several of the luminophores which undergo a change in distribution upon activation or deactivation of the intracellular signalling pathway under study.

15 **Construction and testing of probes**

In general, a probe, i.e. a "GeneX"-GFP fusion or a GFP-"GeneX" fusion, is constructed using PCR with "GeneX"-specific primers followed by a cloning step to fuse "GeneX" in frame with GFP. The fusion may contain a short vector derived sequence between "GeneX" and GFP (e.g. part of a multiple cloning site region in the plasmid) resulting in a peptide linker between "GeneX" and GFP in the resulting fusion protein. 20

Detailed stepwise procedure:

- Identifying the sequence of the gene. This is most readily done by searching a depository of genetic information, e.g. the GenBank Sequence Database, which is widely available and 25 routinely used by molecular biologists. In the specific examples below the GenBank Accession number of the gene in question is provided.

- Design of gene-specific primers. Inspection of the sequence of the gene allows design of gene-specific primers to be used in a PCR reaction. Typically, the top-strand primer encompasses the ATG start codon of the gene and the following ca. 20 nucleotides, while the bottom-strand primer encompasses the stop codon and the ca. 20 preceding nucleotides, if 30

the gene is to be fused behind GFP, i.e. a GFP-"GeneX" fusion. If the gene is to be fused in front of GFP, i.e. a "GeneX"-GFP fusion, a stop codon must be avoided. Optionally, the full length sequence of GeneX may not be used in the fusion, but merely the part which localizes and redistributes like GeneX in response to a signal.

5

- In addition to gene-specific sequences, the primers contain at least one recognition sequence for a restriction enzyme, to allow subsequent cloning of the PCR product. The sites are chosen so that they are unique in the PCR product and compatible with sites in the cloning vector. Furthermore, it may be necessary to include an exact number of nucleotides between 10 the restriction enzyme site and the gene-specific sequence in order to establish the correct reading frame of the fusion gene and/or a translation initiation consensus sequence. Lastly, the primers always contain a few nucleotides in front of the restriction enzyme site to allow efficient digestion with the enzyme.
- 15 -Identifying a source of the gene to be amplified. In order for a PCR reaction to produce a product with gene-specific primers, the gene-sequence must initially be present in the reaction, e.g. in the form of cDNA. Information in GenBank or the scientific literature will usually indicate in which tissue(s) the gene is expressed, and cDNA libraries from a great variety of tissues or cell types from various species are commercially available, e.g. from Clontech 20 (Palo Alto), Stratagene (La Jolla) and Invitrogen (San Diego). Many genes are also available in cloned form from The American Type Tissue Collection (Virginia).
- Optimizing the PCR reaction. Several factors are known to influence the efficiency and specificity of a PCR reaction, including the annealing temperature of the primers, the concentration of ions, notably Mg²⁺ and K⁺, present in the reaction, as well as pH of the reaction. 25 If the result of a PCR reaction is deemed unsatisfactory, it might be because the parameters mentioned above are not optimal. Various annealing temperatures should be tested, e.g. in a PCR machine with a built-in temperature gradient, available from e.g. Stratagene (La Jolla), and/or various buffer compositions should be tried, e.g. the OptiPrime buffer system from 30 Stratagene (La Jolla).

- Cloning the PCR product. The vector into which the amplified gene product will be cloned and fused with GFP will already have been taken into consideration when the primers were designed. When choosing a vector, one should at least consider in which cell types the probe subsequently will be expressed, so that the promoter controlling expression of the probe
- 5 is compatible with the cells. Most expression vectors also contain one or more selective markers, e.g. conferring resistance to a drug, which is a useful feature when one wants to make stable transfecants. The selective marker should also be compatible with the cells to be used.
- 10 The actual cloning of the PCR product should present no difficulty as it typically will be a one-step cloning of a fragment digested with two different restriction enzymes into a vector digested with the same two enzymes. If the cloning proves to be problematic, it may be because the restriction enzymes did not work well with the PCR fragment. In this case one could add longer extensions to the end of the primers to overcome a possible difficulty of digestion close to a fragment end, or one could introduce an intermediate cloning step not based on restriction enzyme digestion. Several companies offer systems for this approach, e.g.
- 15 Invitrogen (San Diego) and Clontech (Palo Alto).

Once the gene has been cloned and, in the process, fused with the GFP gene, the resulting product, usually a plasmid, should be carefully checked to make sure it is as expected. The most exact test would be to obtain the nucleotide sequence of the fusion-gene.

Testing the probe

Once a DNA construct for a probe has been generated, its functionality and usefulness may

25 be tested by subjecting it to the following tests:

- Transfecting it into cells capable of expressing the probe. The fluorescence of the cell is inspected soon after, typically the next day. At this point, two features of cellular fluorescence are noted: the intensity and the sub-cellular localization.

The intensity should usually be at least as strong as that of unfused GFP in the cells. If it is not, the sequence or quality of the probe-DNA might be faulty, and should be carefully checked.

- 5 The sub-cellular localization is an indication of whether the probe is likely to perform well. If it localizes as expected for the gene in question, e.g. is excluded from the nucleus, it can immediately go on to a functional test. If the probe is not localized soon after the transfection procedure, it may be because of overexpression at this point in time, as the cell typically will have taken of very many copies of the plasmid, and localization will occur in time, e.g. within
- 10 a few weeks, as plasmid copy number and expression level decreases. If localization does not occur after prolonged time, it may be because the fusion to GFP has destroyed a localization function, e.g. masked a protein sequence essential for interaction with its normal cellular anchor-protein. In this case the opposite fusion might work, e.g. if GeneX-GFP does not work, GFP-GeneX might, as two different parts of GeneX will be affected by the proximity to
- 15 GFP. If this does not work, the proximity of GFP at either end might be a problem, and it could be attempted to increase the distance by incorporating a longer linker between GeneX and GFP in the DNA construct.

- If there is no prior knowledge of localization, and no localization is observed, it may be because the probe should not be localized at this point, because such is the nature of the protein fused to GFP. It should then be subjected to a functional test.
- 20

- In a functional test, the cells expressing the probe are treated with at least one compound known to perturb, usually by activating, the signalling pathway on which the probe is expected to report by redistributing itself within the cell. If the redistribution is as expected, e.g. if prior knowledge tell that it should translocate from location X to location Y, it has passed the first critical test. In this case it can go on to further characterization and quantification of the response.
- 25

- If it does not perform as expected, it may be because the cell lacks at least one component of the signalling pathway, e.g. a cell surface receptor, or there is species incompatibility, e.g. if the probe is modelled on sequence information of a human gene product, and the cell is of hamster origin. In both instances one should identify other cell types for the testing process where these potential problems would not apply.
- 30

If there is no prior knowledge about the pattern of redistribution, the analysis of the redistribution will have to be done in greater depth to identify what the essential and indicative features are, and when this is clear, it can go on to further characterization and quantification of the response. If no feature of redistribution can be identified, the problem might be as mentioned above, and the probe should be retested under more optimal cellular conditions.

5 If the probe does not perform under optimal cellular conditions it's back to the drawing board.

Developing an image-based assay technique

The process of developing an image-based redistribution assay begins with either the unplanned experimental observation that a redistribution phenomenon can be visualised, or the design of a probe specifically to follow a redistribution phenomenon already known to occur. In either event, the first and best exploratory technique is for a trained scientist or technician to observe the phenomenon. Even with the rapid advances in computing technology, the human eye-brain combination is still the most powerful pattern recognition system known, and requires no advance knowledge of the system in order to detect potentially interesting and useful patterns in raw data. This is especially if those data are presented in the form of images, which are the natural "data type" for human visual processing. Because human visual processing operates most effectively in a relatively narrow frequency range, i.e., we cannot see either very fast or very slow changes in our visual field, it may be necessary to record the data and play it back with either time dilation or time compression.

10 Some luminescence phenomena cannot be seen directly by the human eye. Examples include polarization and fluorescence lifetime. However, with suitable filters or detectors, these signals can be recorded as images or sequences of images and displayed to the human in the fashion just described. In this way, patterns can be detected and the same methods can be applied.

15 Once the redistribution has been determined to be a reproducible phenomenon, one or more data sets are generated for the purpose of developing a procedure for extracting the quantitative information from the data. In parallel, the biological and optical conditions are determined which will give the best quality raw data for the assay. This can become an iterative process; it may be necessary to develop a quantitative procedure in order to assess the effect 20 on the assay of manipulating the assay conditions.

The data sets are examined by a person or persons with knowledge of the biological phenomenon and skill in the application of image processing techniques. The goal of this exercise is to determine or at least propose a method which will reduce the image or sequence of images constituting the record of a "response" to a value corresponding to the degree of the response. Using either interactive image processing software or an image processing tool-box and a programming language, the method is encoded as a procedure or algorithm which takes the image or images as input and generates the degree of response (in any units) as its output. Some of the criteria for evaluating the validity of a particular procedure are:

- Does the degree of the response vary in a biologically significant fashion, i.e., does it show the known or putative dependence on the concentration of the stimulating agent or condition?
- Is the degree of response reproducible, i.e., does the same concentration or level of stimulating agent or condition give the same response with an acceptable variance?
- Is the dynamic range of the response sufficient for the purpose of the assay? If not, can a change in the procedure or one of its parameters improve the dynamic range?
- Does the procedure exhibit any clear "pathologies", i.e., does it give ridiculous values for the response if there are commonly occurring imperfections in the imaging process? Can these pathologies be eliminated, controlled, or accounted for?
- Can the procedure deal with the normal variation in the number and/or size of cells in an image?

In some cases the method may be obvious; in others, a number of possible procedures may suggest themselves. Even if one method appears clearly superior to others, optimisation of parameters may be required. The various procedures are applied to the data set and the criteria suggested above are determined, or the single procedure is applied repeatedly with adjustment of the parameter or parameters until the most satisfactory combination of signal, noise, range, etc. are arrived at. This is equivalent to the calibration of any type of single-channel sensor.

The number of ways of extracting a single value from an image are extremely large, and thus an intelligent approach must be taken to the initial step of reducing this number to a small, finite number of possible procedures. This is not to say that the procedure arrived at is

necessarily the best procedure - but a global search for the best procedure is simply out of the question due to the sheer number of possibilities involved.

Image-based assays are no different than other assay techniques in that their usefulness is characterised by parameters such as the specificity for the desired component of the

- 5 sample, the dynamic range, the variance, the sensitivity, the concentration range over which the assay will work, and other such parameters. While it is not necessary to characterise each and every one of these before using the assay, they represent the only way to compare one assay with another.

10 Example: Developing a Quantitative assay for GLUT4 Translocation

GLUT4 is a member of the class of glucose transporter molecules which are important in cellular glucose uptake. It is known to translocate to the plasma membrane under some conditions of stimulation of glucose uptake. The ability to visualize the glucose uptake response noninvasively, without actually measuring glucose uptake, would be a very useful
15 assay for anyone looking for, for example, treatments for type II diabetes.

- A CHO cell line which stably expressed the human insulin receptor was used as the basis for a new cell line which stably expressed a fusion between GLUT4 and GFP. This cell line was expected to show translocation of GLUT4 to the plasma membrane as visualized by the movement of the GFP. The translocation could definitely be seen in the form of the appearance
20 of local increases in the fluorescence in regions of the plasma membrane which had a characteristic shape or pattern. This is shown in Figure 12.

- These objects became known as "snircles", and the phenomenon of their appearance as "snircling". In order to quantitate their appearance, a method had to be found to isolate them as objects in the image field, and then enumerate them, measure their area, or determine
25 some parameter about them which correlated in a dose-dependent fashion with the concentration of insulin to which the cells had been exposed. In order to separate the snircles, a binarization procedure was applied in which one copy of the image smoothed with a relatively severe gaussian kernel ($\sigma = 2.5$) was subtracted from another copy to which only a relatively light gaussian smooth had been applied ($\sigma = 0.5$). The resultant image was rescaled to its min/max range, and an automatic threshold was applied to divide the image into two levels. The thresholded image contains a background of one value all found object with another value. The found objects were first filtered through a filter to remove objects far too
30

large and far too small to be snircles. The remaining objects, which represent snircles and other artifacts from the image with approximately the same size and intensity characteristics as snircles, are passed into a classification procedure which has been previously trained with many images of snircles to recognize snircles and exclude the other artifacts. The result of 5 this procedure is a binary image which shows only the found snircles to the degree to which the classification procedure can accurately identify them. The total area of the snircles is then summed and this value is the quantitative measure of the degree of snircling for that image.

10 **Definitions:**

In the present specification and claims, the term "an influence" covers any influence to which the cellular response comprises a redistribution. Thus, e.g., heating, cooling, high pressure, low pressure, humidifying, or drying are influences on the cellular response on which the resulting redistribution can be quantified, but as mentioned above, perhaps the most important 15 influences are the influences of contacting or incubating the cell or cells with substances which are known or suspected to exert an influence on the cellular response involving a redistribution contribution. In another embodiment of the invention the influence could be substances from a compound drug library.

20 In the present context, the term "green fluorescent protein" is intended to indicate a protein which, when expressed by a cell, emits fluorescence upon exposure to light of the correct excitation wavelength (cf. [(Chalfie et al. 1994)]). In the following, GFP in which one or more amino acids have been substituted, inserted or deleted is most often termed "modified GFP". "GFP" as used herein includes wild-type GFP derived from the jelly-fish *Aequorea victoria* 25 and modifications of GFP, such as the blue fluorescent variant of GFP disclosed by Heim et al. (1994). Proc.Natl.Acad.Sci. 91:12501, and other modifications that change the spectral properties of the GFP fluorescence, or modifications that exhibit increased fluorescence when expressed in cells at a temperature above about 30°C described in PCT/DK96/00051, published as WO 97/11094 on 27 March 1997 and hereby incorporated by reference, and 30 which comprises a fluorescent protein derived from *Aequorea* Green Fluorescent Protein (GFP) or any functional analogue thereof, wherein the amino acid in position 1 upstream from the chromophore has been mutated to provide an increase of fluorescence intensity when the

- fluorescent protein of the invention is expressed in cells. Preferred GFP variants are F64L-GFP, F64L-Y66H-GFP and F64L-S65T-GFP. An especially preferred variant of GFP for use in all the aspects of this invention is EGFP (DNA encoding EGFP which is a F64L-S65T variant with codons optimized for expression in mammalian cells is available from Clontech, 5 Palo Alto, plasmids containing the EGFP DNA sequence, cf. GenBank Acc. Nos. U55762, U55763).

- The term "intracellular signalling pathway" and "signal transduction pathway" are intended to indicate the coordinated intracellular processes whereby a living cell transduce an external or internal signal into cellular responses. Said signal transduction will involve an enzymatic reaction said enzymes include but are not limited to protein kinases, GTPases, ATPases, protein phosphatases, phospholipases. The cellular responses include but are not limited to gene transcription, secretion, proliferation, mechanical activity, metabolic activity, cell death.
- 10
- 15 The term "second messenger" is used to indicate a low molecular weight component involved in the early events of intracellular signal transduction pathways.
- The term "luminophore" is used to indicate a chemical substance which has the property of emitting light either inherently or upon stimulation with chemical or physical means. This includes but is not limited to fluorescence, bioluminescence, phosphorescence, chemiluminescence.
- 20
- 25 The term "mechanically intact living cell" is used to indicate a cell which is considered living according to standard criteria for that particular type of cell such as maintenance of normal membrane potential, energy metabolism, proliferative capability, and has not experienced any physically invasive treatment designed to introduce external substances into the cell such as microinjection.
- 30
- The term "physiologically relevant" ,when applied to an experimentally determined redistribution of an intracellular component, as measured by a change in the luminescence properties or distribution, is used to indicate that said redistribution can be explained in terms of the underlying biological phenomenon which gives rise to the redistribution.

The terms "image processing" and "image analysis" are used to describe a large family of digital data analysis techniques or combination of such techniques which reduce ordered arrays of numbers (images) to quantitative information describing those ordered arrays of numbers. When said ordered arrays of numbers represent measured values from a physical process, the quantitative information derived is therefore a measure of the physical process.

The term "fluorescent probe" is used to indicate a fluorescent fusion polypeptide comprising a GFP or any functional part thereof which is N- or C-terminally fused to a biologically active polypeptide as defined herein, optionally via a peptide linker consisting of one or more amino acid residues, where the size of the linker peptide in itself is not critical as long as the desired functionality of the fluorescent probe is maintained. A fluorescent probe according to the invention is expressed in a cell and basically mimics the physiological behaviour of the biologically active polypeptide moiety of the fusion polypeptide.

The term "mammalian cell" is intended to indicate any living cell of mammalian origin. The cell may be an established cell line, many of which are available from The American Type Culture Collection (ATCC, Virginia, USA) or a primary cell with a limited life span derived from a mammalian tissue, including tissues derived from a transgenic animal, or a newly established immortal cell line derived from a mammalian tissue including transgenic tissues, or a hybrid cell or cell line derived by fusing different celltypes of mammalian origin e.g. hybridoma cell lines. The cells may optionally express one or more non-native gene products, e.g. receptors, enzymes, enzyme substrates, prior to or in addition to the fluorescent probe. Preferred cell lines include but are not limited to those of fibroblast origin, e.g. BHK, CHO, BALB, or of endothelial origin, e.g. HUVEC, BAE (bovine artery endothelial), CPAE (cow pulmonary artery endothelial) or of pancreatic origin, e.g. RIN, INS-1, MIN6, bTC3, aTC6, bTC6, HIT, or of hematopoietic origin, e.g. adipocyte origin, e.g. 3T3-L1, neuronal/neuroendocrine origin, e.g. AtT20, PC12, GH3, muscle origin, e.g. SKMC, A10, C2C12, renal origin, e.g. HEK 293, LLC-PK1.

The term "hybrid polypeptide" is intended to indicate a polypeptide which is a fusion of at least a portion of each of two proteins, in this case at least a portion of the green fluorescent protein, and at least a portion of a catalytic and/or regulatory domain of a protein kinase. Furthermore a hybrid polypeptide is intended to indicate a fusion polypeptide comprising a

- GFP or at least a portion of the green fluorescent protein that contains a functional fluorophore, and at least a portion of a biologically active polypeptide as defined herein provided that said fusion is not the PKC α -GFP, PKC γ -GFP, and PKC ϵ -GFP disclosed by Schmidt et al. and Sakai et al., respectively. Thus, GFP may be N- or C-terminally tagged to a biologically active polypeptide, optionally via a linker portion or linker peptide consisting of a sequence of one or more amino acids. The hybrid polypeptide or fusion polypeptide may act as a fluorescent probe in intact living cells carrying a DNA sequence encoding the hybrid polypeptide under conditions permitting expression of said hybrid polypeptide.
- 5
- 10 The term "kinase" is intended to indicate an enzyme that is capable of phosphorylating a cellular component.
- The term "protein kinase" is intended to indicate an enzyme that is capable of phosphorylating serine and/or threonine and/or tyrosine in peptides and/or proteins.
- 15 The term "phosphatase" is intended to indicate an enzyme that is capable of dephosphorylating phosphoserine and/or phosphothreonine and/or phosphotyrosine in peptides and/or proteins.
- In the present context, the term "biologically active polypeptide" is intended to indicate a polypeptide affecting intracellular processes upon activation, such as an enzyme which is active in intracellular processes or a portion thereof comprising a desired amino acid sequence which has a biological function or exerts a biological effect in a cellular system. In the polypeptide one or several amino acids may have been deleted, inserted or replaced to alter its biological function, e.g. by rendering a catalytic site inactive. Preferably, the biologically active polypeptide is selected from the group consisting of proteins taking part in an intracellular signalling pathway, such as enzymes involved in the intracellular phosphorylation and dephosphorylation processes including kinases, protein kinases and phosphorylases as defined herein, but also proteins making up the cytoskeleton play important roles in intracellular signal transduction and are therefore included in the meaning of "biologically active polypeptide"
- 20
- 25
- 30

termediary component in a signal transduction pathway. Included in this preferred group of biologically active polypeptides are cAMP dependent protein kinase A.

- The term "a substance having biological activity" is intended to indicate any sample which
- 5 has a biological function or exerts a biological effect in a cellular system. The sample may be a sample of a biological material such as a sample of a body fluid including blood, plasma, saliva, milk, urine, or a microbial or plant extract, an environmental sample containing pollutants including heavy metals or toxins, or it may be a sample containing a compound or mixture of compounds prepared by organic synthesis or genetic techniques.

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- The phrase "any change in fluorescence" means any change in absorption properties, such as wavelength and intensity, or any change in spectral properties of the emitted light, such as a change of wavelength, fluorescence lifetime, intensity or polarisation, or any change in the intracellular localisation of the fluorophore. It may thus be localised to a specific cellular
- 15 component (e.g. organelle, membrane, cytoskeleton, molecular structure) or it may be evenly distributed throughout the cell or parts of the cell.

The phrase "back-tracking of a signal transduction pathway" is intended to indicate.

- The term "organism" as used herein indicates any unicellular or multicellular organism preferably originating from the animal kingdom including protozoans, but also organisms that are
- 20 members of the plant kingdoms, such as algae, fungi, bryophytes, and vascular plants are included in this definition.

The term "nucleic acid" is intended to indicate any type of poly- or oligonucleic acid sequence, such as a DNA sequence, a cDNA sequence, or an RNA sequence.

25

- The term "biologically equivalent" as it relates to proteins is intended to mean that a first protein is equivalent to a second protein if the cellular functions of the two proteins may substitute for each other, e.g. if the two proteins are closely related isoforms encoded by different genes, if they are splicing variants, or allelic variants derived from the same gene, if
- 30 they perform identical cellular functions in different cell types, or in different species. The term "biologically equivalent" as it relates to DNA is intended to mean that a first DNA sequ-

ence encoding a polypeptide is equivalent to a second DNA sequence encoding a polypeptide if the functional proteins encoded by the two genes are biologically equivalent.

The phrase "back-tracking of a signal transduction pathway" is intended to indicate a process
5 for defining more precisely at what level a signal transduction pathway is affected, either by the influence of chemical compounds or a disease state in an organism. Consider a specific signal transduction pathway represented by the bioactive polypeptides A - B - C - D, with signal transduction from A towards D. When investigating all components of this signal transduction pathway compounds or disease states that influence the activity or redistribu-
10 tion of only D can be considered to act on C or downstream of C whereas compounds or disease states that influence the activity or redistribution of C and D, but not of A and B can be considered to act downstream of B.

The term "fixed cells" is used to mean cells treated with a cytological fixative such as glu-
15 taraldehyde or formaldehyde, treatments which serve to chemically cross-link and stabilize soluble and insoluble proteins within the structure of the cell. Once in this state, such proteins cannot be lost from the structure of the now-dead cell.

20

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. CHO cells expressing the PKAc-F64L-S65T-GFP hybrid protein have been treated in HAM's F12 medium with 50 mM forskolin at 37°C. The images of the GFP fluorescence in
25 these cells have been taken at different time intervals after treatment, which were: a) 40 seconds b) 60 seconds c) 70 seconds d) 80 seconds. The fluorescence changes from a punctate to a more even distribution within the (non-nuclear) cytoplasm.

Figure 2. Time-lapse analysis of forskolin induced PKAc-F64L-S65T-GFP redistribution. CHO cells, expressing the PKAc-F64L-S65T-GFP fusion protein were analysed by time-lapse fluorescence microscopy. Fluorescence micrographs were acquired at regular intervals from 2 min before to 8 min after the addition of agonist. The cells were challenged with 1 mM 5 forskolin immediately after the upper left image was acquired (t=0). Frames were collected at the following times: i) 0, ii) 1, iii) 2, iv) 3, v) 4 and vi) 5 minutes. Scale bar 10 mm.

Figure 3. Time-lapse analyses of PKAc-F64L-S65T-GFP redistribution in response to various 10 agonists. The effects of 1 mM forskolin (A), 50 mM forskolin (B), 1mM dbcAMP (C) and 100 mM IBMX (D) (additions indicated by open arrows) on the localisation of the PKAc-F64L-S65T-GFP fusion protein were analysed by time-lapse fluorescence microscopy of CHO/PKAc-F64L-S65T-GFP cells. The effect of addition of 10 mM forskolin (open arrow), followed shortly by repeated washing with buffer (solid arrow), on the localisation of the 15 PKAc-F64L-S65T-GFP fusion protein was analysed in the same cells (E). In a parallel experiment, the effect of adding 10 mM forskolin and 100 mM IBMX (open arrow) followed by repeated washing with buffer containing 100 mM IBMX (solid arrow) was analysed (F). Removing forskolin caused PKAc-F64L-S65T-GFP fusion protein to return to the cytoplasmic aggregates while this is prevented by the continued presence of IBMX (F). The effect of 100 20 nM glucagon (Fig 3G, open arrow) on the localisation of the PKAc-F64L-S65T-GFP fusion protein is also shown for BHK/GR, PKAc-F64L-S65T-GFP cells. The effect of 10 mM norepinephrine (H), solid arrow, on the localisation of the PKAc-F64L-S65T-GFP fusion protein was analysed similarly, in transiently transfected CHO, PKAc-F64L-S65T-GFP cells, pretreated with 10 mM forskolin, open arrow, to increase [cAMP]_i. N.B. in Fig 3H the x-axis counts 25 the image numbers, with 12 seconds between images. The raw data of each experiment consisted of 60 fluorescence micrographs acquired at regular intervals including several images acquired before the addition of buffer or agonist. The charts (A-G) each show a quantification of the response seen through all the 60 images, performed as described in analysis method 2. The change in total area of the highly fluorescent aggregates, relative to 30 the initial area of fluorescent aggregates is plotted as the ordinate in all graphs in Figure 3, versus time for each experiment. Scale bar 10 mm.

Figure 4. Dose response curve (two experiments) for forskolin-induced redistribution of the PKAc-F64L-S65T-GFP fusion.

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Figure 5. Time from initiation of a response to half maximal ($t_{1/2\max}$) and maximal (t_{\max}) PKAc-F64L-S65T-GFP redistribution. The data was extracted from curves such as that shown in "Figure 2." All $t_{1/2\max}$ and t_{\max} values are given as mean \pm SD and are based on a total of 26-30 cells from 2-3 independent experiments for each forskolin concentration. Since the observed 10 redistribution is sustained over time, the t_{\max} values were taken as the earliest time point at which complete redistribution is reached. Note that the values do not relate to the degree of redistribution.

15 Figure 6. Parallel dose response analyses of forskolin induced cAMP elevation and PKAc-F64L-S65T-GFP redistribution. The effects of buffer or 5 increasing concentrations of forskolin on the localisation of the PKAc-F64L-S65T-GFP fusion protein in CHO/PKAc-F64L-S65T-GFP cells, grown in a 96 well plate, were analysed as described above. Computing the ratio of the SD's of fluorescence micrographs taken of the same field of cells, prior to and 30 min 20 after the addition of forskolin, gave a reproducible measure of PKAc-F64L-S65T-GFP redistribution. The graph shows the individual 48 measurements and a trace of their means \pm s.e.m at each forskolin concentration. For comparison, the effects of buffer or 8 increasing concentrations of forskolin on [cAMP], was analysed by a scintillation proximity assay of cells grown under the same conditions. The graph shows a trace of the mean \pm s.e.m of 4 25 experiments expressed in arbitrary units.

Figure 7. BHK cells stably transfected with the human muscarinic (hM1) receptor and the PKCa-F64L-S65T-GFP fusion. Carbachol (100 mM added at 1.0 second) induced a transient redistribution of PKCa-F64L-S65T-GFP from the cytoplasm to the plasma membrane. Images were taken at the following times: a) 1 second before carbachol addition, b) 8.8 seconds 30 after addition and c) 52.8 seconds after addition.

Figure 8. BHK cells stably transfected with the hM1 receptor and PKCa-F64L-S65T-GFP fusion were treated with carbachol (1 mM, 10 mM, 100 mM). In single cells intracellular [Ca²⁺] was monitored simultaneously with the redistribution of PKCa-F64L-S65T-GFP. Data: dashed line indicates the addition times of carbachol. The top panel shows changes in the intracellular Ca²⁺ concentration of individual cells with time for each treatment. The middle panel shows changes in the average cytoplasmic GFP fluorescence for individual cells against time for each treatment. The bottom panel shows changes in the fluorescence of the periphery of single cells, within regions that specifically include the circumferential edge of a cell as seen in normal projection, the regions which offers best chance to monitor changes in the fluorescence intensity of the plasma membrane.

Figure 9. a) The hERK1-F64L-S65T-GFP fusion expressed in HEK293 cells treated with 100 mM of the MEK1 inhibitor PD98059 in HAM F-12 (without serum) for 30 minutes at 37 °C.
15 The nuclei empty of fluorescence during this treatment.
b) The same cells as in (a) following treatment with 10 % foetal calf serum for 15 minutes at 37 °C.
c) Time profiles for the redistribution of GFP fluorescence in HEK293 cells following treatment with various concentrations of EGF in Hepes buffer (HAM F-12 replaced with Hepes
20 buffer directly before the experiment). Redistribution of fluorescence is expressed as the change in the ratio value between areas in nucleus and cytoplasm of single cells. Each time profile is the mean for the changes seen in six single cells.
d) Bar chart for the end-point measurements, 600 seconds after start of EGF treatments, of fluorescence change (nucleus:cytoplasm) following various concentrations of EGF.

25

Figure 10.

a) The SMAD2-EGFP fusion expressed in HEK293 cells starved of serum overnight in HAM F-12. HAM F-12 was then replaced with Hepes buffer pH 7.2 immediately before the experiment. Scale bar is 10 mm.
30 b) HEK 293 cells expressing the SMAD2-EGFP fusion were treated with various concentration of TGF-beta as indicated, and the redistribution of fluorescence monitored against time.

The time profile plots represent increases in fluorescence within the nucleus, normalised to starting values in each cell measured. Each trace is the time profile for a single cell nucleus.

c) A bar chart representing the end-point change in fluorescence within nuclei (after 850 seconds of treatment) for different concentrations of TGF-beta. Each bar is the value for a

5 single nucleus in each treatment.

Figure 11. The VASP-F64L-S65T-GFP fusion in CHO cells stably transfected with the human insulin receptor. The cells were starved for two hours in HAM F-12 without serum, then treated with 10% foetal calf serum. The image shows the resulting redistribution of fluorescence after 15 minutes of treatment. GFP fluorescence becomes localised in structures identified as focal adhesions along the length of actin stress fibres.

10 Figure 12. Time lapse recording GLUT4-GFP redistribution in CHO-HIR cells. Time indicates minutes after the addition of 100 nM insulin.

EXAMPLE 1

- 5 Construction, testing and implementation of an assay for cAMP based on PKA activation in real time within living cells.
Useful for monitoring the activity of signalling pathways which lead to altered concentrations of cAMP, e.g. activation of G-protein coupled receptors which couple to G-proteins of the G_s or G_i class.

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The catalytic subunit of the murine cAMP dependent protein kinase (PKAc) was fused C-terminally to a F64L-S65T derivative of GFP. The resulting fusion (PKAc-F64L-S65T-GFP) was used for monitoring *in vivo* the translocation and thereby the activation of PKA.

Construction of the PKAc-F64L-S65T-GFP fusion:

- 15 Convenient restriction endonuclease sites were introduced into the cDNAs encoding murine PKAc (Gen Bank Accession number: M12303) and F64L-S65T-GFP (sequence disclosed in WO 97/11094) by polymerase chain reaction (PCR). The PCR reactions were performed according to standard protocols with the following primers:

- 5'PKAc: TTggACACAAgCTTTggACACCCTCAggATATgggAACgCCgCCgCCgCCAAg
20 (SEQ ID NO:3),
3'PKAc: gTCATCTTCTCgAgTCTTCAggCgCgCCCAAACTCAgTAAACTCCTTgCCACAC
(SEQ ID NO:4),
5'GFP: TTggACACAAgCTTTggACACggCgCgCCATgAgTAAAggAgAAgAACTTTTC (SEQ ID NO:1),
25 3'GFP: gTCATCTTCTCgAgTCTTACTCCTgAggTTTgTATAgTTCATCCATgCCATgT (SEQ ID NO:2).

The PKAc amplification product was then digested with HindIII+Ascl and the F64L-S65T-GFP product with Ascl+Xhol. The two digested PCR products were subsequently ligated with a HindIII+Xhol digested plasmid (pZeoSV® mammalian expression vector, Invitrogen, San Diego, CA, USA). The resulting fusion construct (SEQ ID NO:68 & 69) was under control of the SV40 promoter.

5 Transfection and cell culture conditions.

- Chinese hamster ovary cells (CHO), were transfected with the plasmid containing the PKAc-F64L-S65T-GFP fusion using the calcium phosphate precipitate method in HEPES-buffered saline (Sambrook et al., 1989). Stable transfectants were selected using 1000 mg Zeocin/ml (Invitrogen) in the growth medium (DMEM with 1000 mg glucose/l, 10 % fetal bovine serum (FBS), 100 mg penicillin-streptomycin mixture ml⁻¹, 2 mM L-glutamine purchased from Life Technologies Inc., Gaithersburg, MD, USA). Untransfected CHO cells were used as the control. To assess the effect of glucagon on fusion protein translocation, the PKAc-F64L-S65T-GFP fusion was stably expressed in baby hamster kidney cells overexpressing the human glucagon receptor (BHK/GR cells). Untransfected BHK/GR cells were used as the control. Expression of GR was maintained with 500 mg G418/ml (Neo marker) and PKAc-F64L-S65T-GFP was maintained with 500 mg Zeocin/ml (Sh b/e marker). CHO cells were also simultaneously co-transfected with vectors containing the PKAc-F64L-S65T-GFP fusion and the human a2a adrenoceptor (hARa2a).
- 10 15 20 25
- For fluorescence microscopy, cells were allowed to adhere to Lab-Tek chambered cover-glasses (Nalge Nunc Int., Naperville, IL, USA) for at least 24 hours and cultured to about 80% confluence. Prior to experiments, the cells were cultured over night without selection pressure in HAM F-12 medium with glutamax (Life Technologies), 100 mg penicillin-streptomycin mixture ml⁻¹ and 0.3 % FBS. This medium has low autofluorescence enabling fluorescence microscopy of cells straight from the incubator.

Monitoring activity of PKA activity in real time:

- Image acquisition of live cells were gathered using a Zeiss Axiovert 135M fluorescence microscope fitted with a Fluar 40X, NA: 1.3 oil immersion objective and coupled to a Photometrics CH250 charged coupled device (CCD) camera. The cells were illuminated with a 100 W HBO arc lamp. In the light path was a 470±20 nm excitation filter, a 510 nm dichroic mirror
- 30

and a 515 ± 15 nm emission filter for minimal image background. The cells were kept and monitored to be at 37°C with a custom built stage heater.

Images were processed and analyzed in the following manner:

Method 1: Stepwise procedure for quantitation of translocation of PKA:

- 5 1. The image was corrected for dark current by performing a pixel-by-pixel subtraction of a dark image (an image taken under the same conditions as the actual image, except the camera shutter is not allowed to open).
- 10 2. The image was corrected for non-uniformity of the illumination by performing a pixel-by-pixel ratio with a flat field correction image (an image taken under the same conditions as the actual image of a uniformly fluorescent specimen).
- 15 3. The image histogram, i.e., the frequency of occurrence of each intensity value in the image, was calculated.
4. A smoothed, second derivative of the histogram was calculated and the second zero is determined. This zero corresponds to the inflection point of the histogram on the high side of the main peak representing the bulk of the image pixel values.
5. The value determined in step 4 was subtracted from the image. All negative values were discarded.
6. The variance (square of the standard deviation) of the remaining pixel values was determined. This value represents the "response" for that image.
- 20 7. Scintillation proximity assay (SPA) for independent quantitation of cAMP:

Method 2: Alternative method for quantitation of PKA redistribution:

1. The fluorescent aggregates are segmented from each image using an automatically found threshold based on the maximisation of the information measure between the object and background. The *a priori* entropy of the image histogram is used as the information measure.
 2. The area of each image occupied by the aggregates is calculated by counting pixels in the segmented areas.
 3. The value obtained in step 2 for each image in a series, or treatment pair, is normalised to the value found for the first (unstimulated) image collected. A value of zero (0) indicates no redistribution of fluorescence from the starting condition. A value of one (1) by this method equals full redistribution.
- 15 Cells were cultured in HAM F-12 medium as described above, but in 96-well plates. The medium was exchanged with Ca²⁺-HEPES buffer including 100 mM IBMX and the cells were stimulated with different concentrations of forskolin for 10 min. Reactions were stopped with addition of NaOH to 0.14 M and the amount of cAMP produced was measured with the cAMP-SPA kit, RPA538 (Amersham) as described by the manufacturer.
- 20 Manipulating intracellular levels of cAMP to test the PKAc-F64L-S65T-GFP fusion.
- The following compounds were used to vary cAMP levels: Forskolin, an activator of adenylyl cyclase; dbcAMP, a membrane permeable cAMP analog which is not degraded by phosphodiesterase; IBMX, an inhibitor of phosphodiesterase.
- 25 CHO cells stably expressing the PKAc-F64L-S65T-GFP, showed a dramatic translocation of the fusion protein from a punctate distribution to an even distribution throughout the cytoplasm following stimulation with 1 mM forskolin (n=3), 10 mM forskolin (n=4) and 50 mM forskolin (n=4) (Fig 1), or dbcAMP at 1mM (n=6).
- Fig. 2 shows the progression of response in time following treatment with 1 mM forskolin.

Fig. 3 gives a comparison of the average temporal profiles of fusion protein redistribution and a measure of the extent of each response to the three forskolin concentrations (Fig. 3A, E, B), and to 1 mM dbcAMP (fig 3C) which caused a similar but slower response, and to addition of 100 mM IBMX (n=4, Fig. 3D) which also caused a slow response, even in the absence of adenylate cyclase stimulation. Addition of buffer (n=2) had no effect (data not shown).

As a control for the behavior of the fusion protein, F64L-S65T-GFP alone was expressed in CHO cells and these were also given 50 mM forskolin (n=5); the uniform diffuse distribution characteristic of GFP in these cells was unaffected by such treatment (data not shown).

The forskolin induced translocation of PKAc-F64L-S65T-GFP showed a dose-response relationship (Fig 4 and 6), see quantitative procedures above.

Reversibility of PKAc-F64L-S65T-GFP translocation.

The release of the PKAc probe from its cytoplasmic anchoring hotspots was reversible. Washing the cells repeatedly (5-8 times) with buffer after 10 μ M forskolin treatment completely restored the punctate pattern within 2-5 min (n=2, Fig. 3E). In fact the fusion protein returned to a pattern of fluorescent cytoplasmic aggregates virtually indistinguishable from that observed before forskolin stimulation.

To test whether the return of fusion protein to the cytoplasmic aggregates reflected a decreased [cAMP]_i, cells were treated with a combination of 10 mM forskolin and 100 mM IBMX (n=2) then washed repeatedly (5-8 times) with buffer containing 100 mM IBMX (Fig. 3F). In these experiments, the fusion protein did not return to its prestimulatory localization after removal of forskolin.

Testing the PKA-F64L-S65T-GFP probe with physiologically relevant agents.

To test the probe's response to receptor activation of adenylate cyclase, BHK cells stably transfected with the glucagon receptor and the PKA-F64L-S65T-GFP probe were exposed to glucagon stimulation. The glucagon receptor is coupled to a G_s protein which activates adenylate cyclase, thereby increasing the cAMP level. In these cells, addition of 100 nM glucagon (n=2) caused the release of the PKA-F64L-S65T-GFP probe from the cytoplasmic aggregates and a resulting translocation of the fusion protein to a more even cytoplasmic

distribution within 2-3 min (Fig. 3G). Similar but less pronounced effects were seen at lower glucagon concentrations (n=2, data not shown). Addition of buffer (n=2) had no effect over time (data not shown).

Transiently transfected CHO cells expressing hARa2a and the PKA-F64L-S65T-GFP probe were treated with 10 mM forskolin for 7.5 minutes, then, in the continued presence of forskolin, exposed to 10 mM norepinephrine to stimulate the exogenous adrenoreceptors, which couple to a G_i protein, which inhibit adenylate cyclase. This treatment led to reappearance of fluorescence in the cytoplasmic aggregates indicative of a decrease in [cAMP]_i (Fig. 3H).

10

Fusion protein translocation correlated with [cAMP]_i

As described above, the time it took for a response to come to completion was dependent on the forskolin dose (Fig. 5) In addition the degree of responses was also dose dependent. To test the PKA-F64L-S65T-GFP fusion protein translocation in a semi high through-put system, CHO cells stably transfected with the PKA-F64L-S65T-GFP fusion was stimulated with buffer and 5 increasing doses of forskolin (n=8). Using the image analysis algorithm described above (Method 1), a dose response relationship was observed in the range from 0.01-50 mM forskolin (Fig. 6). A half maximal stimulation was observed at about 2 mM forskolin. In parallel, cells were stimulated with buffer and 8 increasing concentrations of forskolin (n=4) in the range 0.01-50 mM. The amount of cAMP produced was measured in an SPA assay. A steep increase was observed between 1 and 5 mM forskolin coincident with the steepest part of the curve for fusion protein translocation (also Fig. 6)

25 EXAMPLE 2

Quantitation of redistribution in real-time within living cells.

Probe for detection of PKC activity in real time within living cells:

Construction of PKC-GFP fusion:

The probe was constructed by ligating two restriction enzyme treated polymerase chain reaction (PCR) amplification products of the cDNA for murine PKC α (GenBank Accession number: M25811) and F64L-S65T-GFP (sequence disclosed in WO 97/11094) respectively. Taq® polymerase and the following oligonucleotide primers were used for PCR;

- 5' mPKC α : TTggACACAAgCTTggACACCCTCAggATATggCTgACgTTTACCCggCCAACg (SEQ ID NO:5),
- 3' mPKC α : gTCATCTTCTCgAgTCTTCAggCgCgCCCTACTgCACTTgCAAgtATTgggTgC (SEQ ID NO:6),
- 5' F64L-S65T-GFP: TTggACACAAgCTTggACACggCgCgCCATgAgTAAAaggAgAAgAACTT-TTC (SEQ ID NO:1),
- 3' F64L-S65T-GFP: gTCATCTTCTCgAgTCTTACTCCTgAggTTTgTATAgTTCATCCATgC-CATgT (SEQ ID NO:2).

The hybrid DNA strand was inserted into the pZeoSV® mammalian expression vector as a HindIII-Xhol cassette as described in example 1.

15 Cell Culture:

- BHK cells expressing the human M1 receptor under the control of the inducible metallothionein promoter and maintained with the dihydrofolate reductase marker were transfected with the PKC α -F64L-S65T-GFP probe using the calcium phosphate precipitate method in HEPES buffered saline (HBS [pH 7.10]). Stable transfectants were selected using 20 1000 µg Zeocin®/ml in the growth medium (DMEM with 1000 mg glucose/l, 10 % foetal bovine serum (FBS), 100 mg penicillin-streptomycin mixture ml-1, 2 mM l-glutamine). The hM1 receptor and PKC α -F64L-S65T-GFP fusion protein were maintained with 500 nM methotrexate and 500 µg Zeocin®/ml respectively. 24 hours prior to any experiment, the cells were transferred to HAM F-12 medium with glutamax, 100 µg penicillin-streptomycin 25 mixture ml⁻¹ and 0.3 % FBS. This medium relieves selection pressure, gives a low induction of signal transduction pathways and has a low autofluorescence at the relevant wavelength enabling fluorescence microscopy of cells straight from the incubator.

Monitoring the PKC activity in real time:

- Digital images of live cells were gathered using a Zeiss Axiovert 135M fluorescence microscope fitted with a 40X, NA: 1.3 oil immersion objective and coupled to a Photometrics

CH250 charged coupled device (CCD) camera. The cells were illuminated with a 100 W arc lamp. In the light path was a 470 ± 20 nm excitation filter, a 510 nm dichroic mirror and a 515 ± 15 nm emission filter for minimal image background. The cells were kept and monitored to be at 37°C with a custom built stage heater.

- 5 Images were analyzed using the IPLab software package for Macintosh.

Upon stimulation of the M1-BHK cells, stably expressing the PKC α -F64L-S65T-GFP fusion, with carbachol we observed a dose-dependent transient translocation from the cytoplasm to the plasma membrane (Fig. 7a,b,c). Simultaneous measurement of the cytosolic free calcium concentration shows that the carbachol-induced calcium mobilisation precedes the

- 10 translocation (Fig. 8).

Stepwise procedure for quantitation of translocation of PKC:

1. The image was corrected for dark current by performing a pixel-by-pixel subtraction of a dark image (an image taken under the same conditions as the actual image, except the camera shutter is not allowed to open).
- 15 2. The image was corrected for non-uniformity of the illumination by performing a pixel-by-pixel ratio with a flat field correction image (an image taken under the same conditions as the actual image of a uniformly fluorescent specimen).
3. A copy of the image was made in which the edges are identified. The edges in the image are found by a standard edge-detection procedure – convolving the image with a kernel
- 20 which removes any large-scale unchanging components (i.e., background) and accentuates any small-scale changes (i.e., sharp edges). This image was then converted to a binary image by threshholding. Objects in the binary image which are too small to represent the edges of cells were discarded. A dilation of the binary image was performed to close any gaps in the image edges. Any edge objects in the image which were in contact with the borders of the image are discarded. This binary image represents the edge mask.
- 25 4. Another copy of image was made via the procedure in step 3. This copy was further processed to detect objects which enclose "holes" and setting all pixels inside the holes to the binary value of the edge, i.e., one. This image represents the whole cell mask.
5. The original image was masked with the edge mask from step 3 and the sum total of all
- 30 pixel values is determined.

6. The original image was masked with the whole cell mask from step 4 and the sum total of all pixel values was determined.
7. The value from step 5 was divided by the value from step 6 to give the final result, the fraction of fluorescence intensity in the cells which was localized in the edges.

5

EXAMPLE 3

Probes for detection of mitogen activated protein kinase Erk1 redistribution.

Useful for monitoring signalling pathways involving MAPK, e.g. to identify compounds which
10 modulate the activity of the pathway in living cells.

Erk1, a serine/threonine protein kinase, is a component of a signalling pathway which is activated by e.g. many growth factors.

Probes for detection of ERK-1 activity in real time within living cells:

15 The extracellular signal regulated kinase (ERK-1, a mitogen activated protein kinase, MAPK) is fused N- or C-terminally to a derivative of GFP. The resulting fusions expressed in different mammalian cells are used for monitoring *in vivo* the nuclear translocation, and thereby the activation, of ERK1 in response to stimuli that activate the MAPK pathway.

a) Construction of murine ERK1 - F64L-S65T-GFP fusion:

20 Convenient restriction endonuclease sites are introduced into the cDNAs encoding murine ERK1 (GenBank Accession number: Z14249) and F64L-S65T-GFP (sequence disclosed in WO 97/11094) by polymerase chain reaction (PCR). The PCR reactions are performed according to standard protocols with the following primers:

5'ERK1: TTggACACAAgCTTTggACACCCTCAggATATggCggCggCggCggCggCTCCgggggg-

25 gCgggg (SEQ ID NO:7),

3'ERK1: gTCATCTTCTCgAgTCTTCAggCgCgCCCggggCCCTCTggCgCCCCCTggCTgg
(SEQ ID NO:8),

5'F64L-S65T-GFP: TTggACACAAgCTTTggACACggCgCgCCATgAgTAAAggAgAAgAACTT-TTC (SEQ ID NO:1)

5 3'F64L-S65T-GFP: gTCATCTTCTCgAgTCTTACTCCTgAggTTTgTATAgTTCATCCATg-CATgT (SEQ ID NO:2)

To generate the mERK1-F64L-S65T-GFP (SEQ ID NO:56 & 57) fusion the ERK1 amplification product is digested with HindIII+Ascl and the F64L-S65T-GFP product with Ascl+Xhol. To generate the F64L-S65T-GFP-mERK1 fusion the ERK1 amplification product is then digested with HindIII+Bsu36I and the F64L-S65T-GFP product with Bsu36I+Xhol. The two pairs of digested PCR products are subsequently ligated with a HindIII+Xhol digested plasmid (pZeoSV® mammalian expression vector, Invitrogen, San Diego, CA, USA). The resulting fusion constructs are under control of the SV40 promoter.

15 b) The human Erk1 gene (GenBank Accession number: X60188) was amplified using PCR according to standard protocols with primers Erk1-top (SEQ ID NO:9) and Erk1-bottom/+stop (SEQ ID NO:10). The PCR product was digested with restriction enzymes EcoRI and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with EcoRI and BamH1. This produces an EGFP-Erk1 fusion
20 (SEQ ID NO:38 &39) under the control of a CMV promoter.

The plasmid containing the EGFP-Erk1 fusion was transfected into HEK293 cells employing the FUGENE transfection reagent (Boehringer Mannheim). Prior to experiments the cells were grown to 80%-90% confluence 8 well chambers in DMEM with 10% FCS. The cells were washed in plain HAM F-12 medium (without FCS), and then incubated for 30-60 minutes in plain HAM F-12 (without FCS) with 100 micromolar PD98059, an inhibitor of MEK1, a kinase which activates Erk1; this step effectively empties the nucleus of EGFP-Erk1. Just before starting the experiment, the HAM F-12 was replaced with Hepes buffer following a wash with Hepes buffer. This removes the PD98059 inhibitor; if blocking of MEK1 is still wanted
30 (e.g. in control experiments), the inhibitor is included in the Hepes buffer.

The experimental setup of the microscope was as described in example 1.

60 images were collected with 10 seconds between each, and with the test compound added after image number 10.

5 Addition of EGF (1-100 nM) caused within minutes a redistribution of EGFP-Erk1 from the cytoplasm into the nucleus (Fig. 9a,b).

10 The response was quantitated as described below and a dose-dependent relationship between EGF concentration and nuclear translocation of EGFP-Erk1 was found (Fig. 9c,d). Redistribution of GFP fluorescence is expressed in this example as the change in the ratio value between areas in nuclear versus cytoplasmic compartments of the cell. Each time profile is the average of nuclear to cytoplasmic ratios from six cells in each treatment.

EXAMPLE 4:

Probes for detection of Erk2 redistribution.

15 Useful for monitoring signalling pathways involving MAPK, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Erk2, a serine/threonine protein kinase, is closely related to Erk1 but not identical; it is a component of a signalling pathway which is activated by e.g. many growth factors.

20 a) The rat Erk2 gene (GenBank Accession number: M64300) was amplified using PCR according to standard protocols with primers Erk2-top (SEQ ID NO:11) and Erk2-bottom/+stop (SEQ ID NO:13) The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-Erk2 fusion (SEQ ID NO:40 &41) under the control of a CMV promoter.

25 b) The rat Erk2 gene (GenBank Accession number: M64300) was amplified using PCR according to standard protocols with primers (SEQ ID NO:11) Erk2-top and Erk2-bottom/-stop (SEQ ID NO:12). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produces an Erk2-EGFP fusion (SEQ ID NO:58 &59) under the control of a CMV promoter.

The resulting plasmids were transfected into CHO cells and BHK cells. The cells were grown under standard conditions. Prior to experiments, the cells were starved in medium without serum for 48-72 hours. This led to a predominantly cytoplasmic localization of both probes,
5 especially in BHK cells. 10% fetal calf serum was added to the cells and the fluorescence of the cells was recorded as explained in example 3. Addition of serum caused the probes to redistribute into the nucleus within minutes of addition of serum.

EXAMPLE 5:

10 Probes for detection of Smad2 redistribution.

Useful for monitoring signalling pathways activated by some members of the transforming growth factor-beta family, e.g. to identify compounds which modulate the activity of the pathway in living cells.

15 Smad 2, a signal transducer, is a component of a signalling pathway which is induced by some members of the TGFbeta family of cytokines.

a) The human Smad2 gene (GenBank Accession number: AF027964) was amplified using PCR according to standard protocols with primers Smad2-top (SEQ ID NO:24) and Smad2-bottom/+stop (SEQ ID NO:26). The PCR product was digested with restriction enzymes E-
20 coR1 and Acc65I, and ligated into pEGFP-C1 (Clontech; Palo Alto; GenBank Accession number U55763) digested with EcoR1 and Acc65I. This produces an EGFP-Smad2 fusion (SEQ ID NO:50&51) under the control of a CMV promoter.

b) The human Smad2 gene (GenBank Accession number: AF027964) was amplified using PCR according to standard protocols with primers Smad2-top (SEQ ID NO:24) and Smad2-bottom/-stop (SEQ ID NO:25). The PCR product was digested with restriction enzymes E-
25 coR1 and Acc65I, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and Acc65I. This produces a Smad2-EGFP fusion (SEQ ID NO:74 &75) under the control of a CMV promoter.

30 The plasmid containing the EGFP-Smad2 fusion was transfected into HEK293 cells, where it showed a cytoplasmic distribution. Prior to experiments the cells were grown in 8 well Nunc

chambers in DMEM with 10% FCS to 80% confluency and starved overnight in HAM F-12 medium without FCS.

For experiments, the HAM F-12 medium was replaced with Hepes buffer pH 7.2.

The experimental setup of the microscope was as described in example 1.

- 5 90 images were collected with 10 seconds between each, and with the test compound added after image number 5.

- After serum starvation of cells, each nucleus contains less GFP fluorescence than the surrounding cytoplasm (Fig. 10a). Addition of TGFbeta caused within minutes a redistribution of
10 EGFP-Smad2 from the cytoplasm into the nucleus (Fig. 10b).

The redistribution of fluorescence within the treated cells was quantified simply as the fractional increase in nuclear fluorescence normalised to the starting value of GFP fluorescence in the nucleus of each unstimulated cell.

15 EXAMPLE 6:

Probe for detection of VASP redistribution.

Useful for monitoring signalling pathways involving rearrangement of cytoskeletal elements, e.g. to identify compounds which modulate the activity of the pathway in living cells.

- 20 VASP, a phosphoprotein, is a component of cytoskeletal structures, which redistributes in response to signals which affect focal adhesions.

- a) The human VASP gene (GenBank Accession number: Z46389) was amplified using PCR according to standard protocols with primers VASP-top (SEQ ID NO:94) and VASP-bottom/+stop (SEQ ID NO:95). The PCR product was digested with restriction enzymes Hind3 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Hind3and BamH1. This produces an EGFP-VASP fusion (SEQ ID NO:124 & 125) under the control of a CMV promoter.
25

The resulting plasmid was transfected into CHO cells expressing the human insulin receptor using the calcium-phosphate transfection method. Prior to experiments, cells were grown in 8 well Nunc chambers and starved overnight in medium without FCS.

Experiments are performed in a microscope setup as described in example 1.

10% FCS was added to the cells and images were collected. The EGFP-VASP fusion was redistributed from a somewhat even distribution near the periphery into more localized structures, identified as focal adhesion points (Fig. 11).

5

A large number of further GFP fusions have been made or are in the process of being made, as apparent from the following Examples 7-22 which also suggest suitable host cells and substances for activation of the cellular signalling pathways to be monitored and analyzed.

10

EXAMPLE 7:

Probe for detection of actin redistribution.

15 Useful for monitoring signalling pathways involving rearrangement or formation of actin filaments, e.g. to identify compounds which modulate the activity of pathways leading to cytoskeletal rearrangements in living cells.

Actin is a component of cytoskeletal structures, which redistributes in response to very many cellular signals.

20

The actin binding domain of the human alpha-actinin gene (GenBank Accession number: X15804) was amplified using PCR according to standard protocols with primers ABD-top (SEQ ID NO:90) and ABD-bottom/-stop (SEQ ID NO:91). The PCR product was digested with restriction enzymes Hind3 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto;

25 GenBank Accession number U55762) digested with Hind3 and BamH1. This produced an actin-binding-domain-EGFP fusion (SEQ ID NO:128 &129) under the control of a CMV promoter.

The resulting plasmid was transfected into CHO cells expressing the human insulin receptor. Cells were stimulated with insulin which caused the actin binding domain-EGFP probe to be-

30 come redistributed into morphologically distinct membrane-associated structures.

Example 8:

Probes for detection of p38 redistribution.

- 5 Useful for monitoring signalling pathways responding to various cellular stress situations, e.g. to identify compounds which modulate the activity of the pathway in living cells, or as a counterscreen.

p38, a serine/threonine protein kinase, is a component of a stress-induced signalling pathway which is activated by many types of cellular stress, e.g. TNFalpha, anisomycin, UV and mi-

10 tomycin C.

- a) The human p38 gene (GenBank Accession number: L35253) was amplified using PCR according to standard protocols with primers p38-top (SEQ ID NO:14) and p38-bottom/+stop (SEQ ID NO: 16). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produced an EGFP-p38 fusion (SEQ ID NO:46 &47) under the control of a CMV promoter.

- b) The human p38 gene (GenBank Accession number: L35253) was amplified using PCR according to standard protocols with primers p38-top (SEQ ID NO:13) and p38-bottom/-stop (SEQ ID NO:15) . The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produced a p38-EGFP fusion (SEQ ID NO:64 &65) under the control of a CMV promoter.

- The resulting plasmids are transfected into a suitable cell line, e.g. HEK293, in which the 25 EGFP-p38 probe and/or the p38-EGFP probe should change its cellular distribution from predominantly cytoplasmic to nuclear within minutes in response to activation of the signalling pathway with e.g. anisomycin.

Example 9:

- 30 Probes for detection of Jnk1 redistribution.

45

Useful for monitoring signalling pathways responding to various cellular stress situations, e.g. to identify compounds which modulate the activity of the pathway in living cells, or as a counterscreen.

- 5 Jnk1, a serine/threonine protein kinase, is a component of a stress-induced signalling pathway different from the p38 described above, though it also is activated by many types of cellular stress, e.g. TNF α , anisomycin and UV.

- 10 a) The human Jnk1 gene (GenBank Accession number: L26318) was amplified using PCR according to standard protocols with primers Jnk-top (SEQ ID NO:17) and Jnk-bottom/+stop (SEQ ID NO:19). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produced an EGFP-Jnk1 fusion (SEQ ID NO:44 &45) under the control of a CMV promoter.
- 15 b) The human Jnk1 gene (GenBank Accession number: L26318) was amplified using PCR according to standard protocols with primers Jnk-top (SEQ ID NO:17) and Jnk-bottom/-stop (SEQ ID NO:18). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produced a Jnk1-EGFP fusion (SEQ ID NO:62 &63) under the control of a CMV promoter.
- 20 The resulting plasmids are transfected into a suitable cell line, e.g. HEK293, in which the EGFP-Jnk1 probe and/or the Jnk1-EGFP probe should change its cellular distribution from predominantly cytoplasmic to nuclear in response to activation of the signalling pathway with e.g. anisomycin.

25

Example 10:

Probes for detection of PKG redistribution.

Useful for monitoring signalling pathways involving changes in cyclic GMP levels, e.g. to identify compounds which modulate the activity of the pathway in living cells.

- 30 PGK, a cGMP-dependent serine/threonine protein kinase, mediates the guanylyl-cyclase/cGMP signal.

- a) The human PKG gene (GenBank Accession number: Y07512) is amplified using PCR according to standard protocols with primers PKG-top (SEQ ID NO:81) and PKG-bottom/+stop (SEQ ID NO:83). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-PKG fusion (SEQ ID NO:134 & 135) under the control of a CMV promoter.
- b) The human PKG gene (GenBank Accession number: Y07512) is amplified using PCR according to standard protocols with primers PKG-top (SEQ ID NO:81) and PKG-bottom/-stop (SEQ ID NO: 82). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produces a PKG-EGFP fusion (SEQ ID NO:136 & 137) under the control of a CMV promoter.
- The resulting plasmids are transfected into a suitable cell line, e.g. A10, in which the EGFP-PKG probe and/or the PKG-EGFP probe should change its cellular distribution from cytoplasmic to one associated with cytoskeletal elements within minutes in response to treatment with agents which raise nitric oxide (NO) levels.

Example 11:

- 20 Probes for detection of IkappaB kinase redistribution.
Useful for monitoring signalling pathways leading to NFkappaB activation, e.g. to identify compounds which modulate the activity of the pathway in living cells.
IkappaB kinase, a serine/threonine kinase, is a component of a signalling pathway which is activated by a variety of inducers including cytokines, lymphokines, growth factors and
25 stress.
- a) The alpha subunit of the human IkappaB kinase gene (GenBank Accession number: AF009225) is amplified using PCR according to standard protocols with primers IKK-top (SEQ ID NO:96) and IKK-bottom/+stop (SEQ ID NO:98). The PCR product is digested with restriction enzymes EcoR1 and Acc65I, and ligated into pEGFP-C1 (Clontech, Palo Alto;

GenBank Accession number U55763) digested with EcoR1 and Acc65I. This produces an EGFP-IkappaB-kinase fusion (SEQ ID NO:120 &121) under the control of a CMV promoter.

b) The alpha subunit of the human IkappaB kinase gene (GenBank Accession number:

AF009225) is amplified using PCR according to standard protocols with primers IKK-top

- 5 (SEQ ID NO:96) and IKK-bottom/-stop (SEQ ID NO:97). The PCR product is digested with restriction enzymes EcoR1 and Acc65I, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and Acc65I. This produces an IkappaB-kinase-EGFP fusion (SEQ ID NO:122 &123) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the

- 10 EGFP-IkappaB-kinase probe and/or the IkappaB-kinase-EGFP probe should achieve a more cytoplasmic distribution within seconds following stimulation with e.g. TNFalpha.

Example 12:

Probes for detection of CDK2 redistribution.

- 15 Useful for monitoring signalling pathways of the cell cycle, e.g. to identify compounds which modulate the activity of the pathway in living cells.

CDK2, a cyclin-dependent serine/threonine kinase, is a component of the signalling system which regulates the cell cycle.

- 20 a) The human CDK2 gene (GenBank Accession number: X61622) is amplified using PCR according to standard protocols with primers CDK2-top (SEQ ID NO:102) and CDK2-bottom/+stop (SEQ ID NO: 104). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-CDK2 fusion (SEQ ID NO:114 &115) under the control of a CMV promoter.

- 25 b) The human CDK2 gene (GenBank Accession number: X61622) is amplified using PCR according to standard protocols with primers CDK2-top (SEQ ID NO:102) and CDK2-bottom/-stop (SEQ ID NO:103). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produces a CDK2-EGFP fusion (SEQ ID NO:112 &113) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. HEK293 in which the EGFP-CDK2 probe and/or the CDK2-EGFP probe should change its cellular distribution from cytoplasmic in contact-inhibited cells, to nuclear location in response to activation with a number of growth factors, e.g. IGF.

5

Example 13:

Probes for detection of Grk5 redistribution.

Useful for monitoring signalling pathways involving desensitization of G-protein coupled receptors, e.g. to identify compounds which modulate the activity of the pathway in living cells.

- 10 Grk5, a G-protein coupled receptor kinase, is a component of signalling pathways involving membrane bound G-protein coupled receptors.
- a) The human Grk5 gene (GenBank Accession number: L15388) is amplified using PCR according to standard protocols with primers Grk5-top (SEQ ID NO:27) and Grk5-bottom/+stop (SEQ ID NO:29). The PCR product is digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with EcoR1 and BamH1. This produces an EGFP-Grk5 fusion (SEQ ID NO:42 &43) under the control of a CMV promoter.
- b) The human Grk5 gene (GenBank Accession number: L15388) is amplified using PCR according to standard protocols with primers Grk5-top (SEQ ID NO:27) and Grk5-bottom/-stop (SEQ ID NO:28). The PCR product is digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produces a Grk5-EGFP fusion (SEQ ID NO:60 &61) under the control of a CMV promoter.
- 25 The resulting plasmids are transfected into a suitable cell line, e.g. HEK293 expressing a rat dopamine D1A receptor, in which the EGFP-Grk5 probe and/or the Grk5-EGFP probe should change its cellular distribution from predominantly cytoplasmic to peripheral in response to activation of the signalling pathway with e.g. dopamine.
- 30 Example 14:

Probes for detection of Zap70 redistribution.

Useful for monitoring signalling pathways involving the T cell receptor, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Zap70, a tyrosine kinase, is a component of a signalling pathway which is active in e.g. T-cell

5 differentiation.

a) The human Zap70 gene (GenBank Accession number: L05148) is amplified using PCR according to standard protocols with primers Zap70-top (SEQ ID NO:105) and Zap70-bottom/+stop (SEQ ID NO:107). The PCR product is digested with restriction enzymes E-
10 coR1 and BamH1, and ligated into pEGFP-C1 (GenBank Accession number U55763) digested with EcoR1 and BamH1. This produces an EGFP-Zap70 fusion (SEQ ID NO:108 &109) under the control of a CMV promoter.

b) The human Zap70 gene (GenBank Accession number: L05148) is amplified using PCR according to standard protocols with primers Zap70-top (SEQ ID NO:105) and Zap70-bottom/-stop (SEQ ID NO:106). The PCR product is digested with restriction enzymes E-
15 coR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produces a Zap70-EGFP fusion (SEQ ID NO:110 &111) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the
20 EGFP-Zap70 probe and/or the Zap70-EGFP probe should change its cellular distribution from cytoplasmic to membrane-associated within seconds in response to activation of the T cell receptor signalling pathway with e.g. antibodies to CD3epsilon.

Example 15:

25 Probes for detection of p85 redistribution.

Useful for monitoring signalling pathways involving PI-3 kinase, e.g. to identify compounds which modulate the activity of the pathway in living cells.

p85alpha is the regulatory subunit of PI3-kinase which is a component of many pathways involving membrane-bound tyrosine kinase receptors and G-protein-coupled receptors.

- a) The human p85alpha gene (GenBank Accession number: M61906) was amplified using PCR according to standard protocols with primers p85-top-C (SEQ ID NO:22) and p85-bottom/+stop (SEQ ID NO:23). The PCR product was digested with restriction enzymes Bgl2 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Bgl2 and BamH1. This produced an EGFP-p85alpha fusion (SEQ ID NO:48 &49) under the control of a CMV promoter.
- b) The human p85alpha gene (GenBank Accession number: M61906) was amplified using PCR according to standard protocols with primers p85-top-N (SEQ ID NO:20) and p85-bottom/-stop (SEQ ID NO:21). The PCR product was digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produced a p85alpha-EGFP fusion (SEQ ID NO:66 &67) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. CHO expressing the human insulin receptor, in which the EGFP-p85 probe and/or the p85-EGFP probe may change its cellular distribution from cytoplasmic to membrane-associated within minutes in response to activation of the receptor with insulin.

Example 16:

- Probes for detection of protein-tyrosine phosphatase redistribution.
- 20 Useful for monitoring signalling pathways involving tyrosine kinases, e.g. to identify compounds which modulate the activity of the pathway in living cells.
- Protein-tyrosine phosphatase1C, a tyrosine-specific phosphatase, is an inhibitory component in signalling pathways involving e.g. some growth factors.
- 25 a) The human protein-tyrosine phosphatase 1C gene (GenBank Accession number: X62055) is amplified using PCR according to standard protocols with primers PTP-top (SEQ ID NO:99) and PTP-bottom/+stop (SEQ ID NO:101). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and EcoR1. This produces an EGFP-PTP fusion (SEQ ID NO:116 &117) under the control of a CMV promoter.

- b) The human protein-tyrosine phosphatase 1C gene (GenBank Accession number: X62055) is amplified using PCR according to standard protocols with primers PTP-top (SEQ ID NO:99) and PTP-bottom/-stop (SEQ ID NO:100). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and EcoR1. This produces a PTP-EGFP fusion (SEQ ID NO:118 &119) under the control of a CMV promoter.
- The resulting plasmids are transfected into a suitable cell line, e.g. MCF-7 in which the EGFP-PTP probe and/or the PTP-EGFP probe should change its cellular distribution from cytoplasm to the plasma membrane within minutes in response to activation of the growth inhibitory signalling pathway with e.g. somatostatin.

Example 17:

Probes for detection of Smad4 redistribution.

- Useful for monitoring signalling pathways involving most members of the transforming growth factor-beta family, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Smad4, a signal transducer, is a common component of signalling pathways induced by various members of the TGFbeta family of cytokines.

- a) The human Smad4 gene (GenBank Accession number: U44378) was amplified using PCR according to standard protocols with primers Smad4-top and Smad4-bottom/+stop (SEQ ID NO:35) . The PCR product was digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with EcoR1 and BamH1. This produce an EGFP-Smad4 fusion (SEQ ID NO:52 &53) under the control of a CMV promoter.
- b) The human Smad4 gene (GenBank Accession number: U44378) was amplified using PCR according to standard protocols with primers Smad4-top (SEQ ID NO:33) and Smad4-bottom/-stop (SEQ ID NO:34). The PCR product was digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produced a Smad4-EGFP fusion (SEQ ID NO:76 &77) under the control of a CMV promoter.

The resulting plasmids are transfected into a cell line, e.g. HEK293 in which the EGFP-Smad4 probe and/or the Smad4-EGFP probe should change its cellular distribution within minutes from cytoplasmic to nuclear in response to activation of the signalling pathway with e.g. TGFbeta.

5

Example 18:

Probes for detection of Stat5 redistribution.

Useful for monitoring signalling pathways involving the activation of tyrosine kinases of the Jak family, e.g. to identify compounds which modulate the activity of the pathway in living

10 cells.

Stat5, signal transducer and activator of transcription, is a component of signalling pathways which are induced by e.g. many cytokines and growth factors.

- a) The human Stat5 gene (GenBank Accession number: L41142) was amplified using PCR according to standard protocols with primers Stat5-top (SEQ ID NO:30) and Stat5-bottom/+stop (SEQ ID NO:32). The PCR product was digested with restriction enzymes Bgl2 and Acc65I, and ligated into pEGFP-C1 (Clontech; Palo Alto; GenBank Accession number U55763) digested with Bgl2 and Acc65I. This produced an EGFP-Stat5 fusion (SEQ ID NO:54 & 55) under the control of a CMV promoter.
- b) The human Stat5 gene (GenBank Accession number: L41142) was amplified using PCR according to standard protocols with primers Stat5-top (SEQ ID NO:30) and Stat5-bottom/-stop (SEQ ID NO:331). The PCR product was digested with restriction enzymes Bgl2 and Acc65I, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Bgl2 and Acc65I. This produced a Stat5-EGFP fusion (SEQ ID NO:78 & 79) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. MIN6 in which the EGFP-Stat5 probe and/or the Stat5-EGFP probe should change its cellular distribution from cytoplasmic to nuclear within minutes in response to activation signalling pathway with e.g. prolactin.

30

Example 19:

Probes for detection of NFAT redistribution.

Useful for monitoring signalling pathways involving activation of NFAT, e.g. to identify compounds which modulate the activity of the pathway in living cells.

- 5 NFAT, an activator of transcription, is a component of signalling pathways which is involved in e.g. immune responses.
 - 10 a) The human NFAT1 gene (GenBank Accession number: U43342) is amplified using PCR according to standard protocols with primers NFAT-top (SEQ ID NO:84) and NFAT-bottom/+stop (SEQ ID NO:86). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and EcoR1. This produces an EGFP-NFAT fusion (SEQ ID NO:130 &131) under the control of a CMV promoter.
 - 15 b) The human NFAT gene (GenBank Accession number: U43342) is amplified using PCR according to standard protocols with primers NFAT-top (SEQ ID NO:84) and NFAT-bottom/-stop (SEQ ID NO:85). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and EcoR1. This produces an NFAT-EGFP fusion (SEQ ID NO:132 &133) under the control of a CMV promoter.
 - 20 The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the EGFP-NFAT probe and/or the NFAT-EGFP probe should change its cellular distribution from cytoplasmic to nuclear within minutes in response to activation of the signalling pathway with e.g. antibodies to CD3epsilon.
- 25 Example 20:

Probes for detection of NFkappaB redistribution.

Useful for monitoring signalling pathways leading to activation of NFkappaB, e.g. to identify compounds which modulate the activity of the pathway in living cells.

NFkappaB, an activator of transcription, is a component of signalling pathways which are responsive to a variety of inducers including cytokines, lymphokines, some immunosuppressive agents.

- 5 a) The human NFkappaB p65 subunit gene (GenBank Accession number: M62399) is amplified using PCR according to standard protocols with primers NFkappaB-top (SEQ ID NO:87) and NFkappaB-bottom/+stop (SEQ ID NO:89). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-NFkappaB fusion (SEQ ID NO:142 & 143) under the control of a CMV promoter.
10 b) The human NFkappaB p65 subunit gene (GenBank Accession number: M62399) is amplified using PCR according to standard protocols with primers NFkappaB-top (SEQ ID NO:87) and NFkappaB-bottom/-stop (SEQ ID NO:88). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; Gen-
15 Bank Accession number U55762) digested with Xho1 and BamH1. This produces an NFkappaB-EGFP fusion (SEQ ID NO:140 & 141) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the EGFP-NFkappaB probe and/or the NFkappaB-EGFP probe should change its cellular distribution from cytoplasmic to nuclear in response to activation of the signalling pathway with
20 e.g. TNFalpha.

Example 21:

Probe for detection of RhoA redistribution.

Useful for monitoring signalling pathways involving RhoA, e.g. to identify compounds which
25 modulate the activity of the pathway in living cells.

RhoA, a small GTPase, is a component of many signalling pathways, e.g. LPA induced cytoskeletal rearrangements.

The human RhoA gene (GenBank Accession number: L25080) was amplified using PCR
30 according to standard protocols with primers RhoA-top (SEQ ID NO:92) and RhoA-bottom/+stop (SEQ ID NO:93). The PCR product was digested with restriction enzymes

Hind3 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Hind3and BamH1. This produced an EGFP-RhoA fusion (SEQ ID NO:126 &127) under the control of a CMV promoter.

The resulting plasmid is transfected into a suitable cell line, e.g. Swiss3T3, in which the

- 5 EGFP-RhoA probe should change its cellular distribution from a reasonably homogenous to a peripheral distribution within minutes of activation of the signalling pathway with e.g. LPA.

Example 22:

Probes for detection of PKB redistribution.

Useful for monitoring signalling pathways involving PKB e.g. to identify compounds which

- 10 modulate the activity of the pathway in living cells.

PKB, a serine/threonine kinase, is a component in various signalling pathways, many of which are activated by growth factors.

- a) The human PKB gene (GenBank Accession number: M63167) is amplified using PCR according to standard protocols with primers PKB-top (SEQ ID NO:36) and PKB-bottom/+stop (SEQ ID NO:80) . The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-PKB fusion (SEQ ID NO:138 & 139) under the control of a CMV promoter.
- b) The human PKB gene (GenBank Accession number: M63167) was amplified using PCR according to standard protocols with primers PKB-top (SEQ ID NO:36) and PKB-bottom/-stop (SEQ ID NO:37) . The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produced a PKB-EGFP fusion (SEQ ID NO:70 &71) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. CHO expressing the human insulin receptor, in which the EGFP-PKB probe and/or the PKB-EGFP probe cycles between cytoplasmic and membrane locations during the activation-deactivation process following addition of insulin. The transition should be apparent within minutes.

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SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) APPLICANT: NovoNordisk, BioImage

10 (ii) TITLE OF THE INVENTION: A Method of Detecting Cellular
Translocation of Biologically Active Polypeptides Using
Fluorescence Imaging

(iii) NUMBER OF SEQUENCES: 143

15 (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: NovoNordisk, BioImage
- (B) STREET: Mørkhøjbygade 28
- (C) CITY: Søborg
- (D) STATE: DK
- 20 (E) COUNTRY: DENMARK
- (F) ZIP: 2860

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

30 (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: , PV&P R
- (B) REGISTRATION NUMBER:
- (C) REFERENCE/DOCKET NUMBER:

35 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGACACAA GCTTTGGACA CGGCGCGCCA TGAGTAAAGG AGAAGAACCTT TTC

53

(2) INFORMATION FOR SEQ ID NO:2:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 GTCATCTTCT CGAGTCTTAC TCCTGAGGTT TGTATAGTTC ATCCATGCCA TGT

53

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGGCAACG CCGCCGCCGC CAAG

54

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC AAACTCAGTA AACTCCTTGC CACAC

55

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGCTGACG TTTACCCGGC CAACG

55

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC TACTGCACCT TGCAAGATTG GGTGC

55

58

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGGACACAA GCTTGGACA CCCTCAGGAT ATGGCGGCGG CGGCGGCGGC TCCGGGGGGC
 GGGG

60

64

15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC GGGGCCCTCT GGCGCCCTG GCTGG

55

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45

TAGAATTCAA CCATGGCGGC GGCGCGGCG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAGGATCCCT AGGGGGCCTC CAGCACTCC

29

55

(2) INFORMATION FOR SEQ ID NO:11:

60

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 TACTCGAGTA ACCATGGCGG CGGCAGCGGC G

31

(2) INFORMATION FOR SEQ ID NO:12:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAGGATCCAT AGATCTGTAT CCTGG

25

25 (2) INFORMATION FOR SEQ ID NO:13:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGGATCCTT AAGATCTGTA TCCTGG

26

(2) INFORMATION FOR SEQ ID NO:14:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

50 ATCTCGAGGG AAAATGTCTC AGGAGAGG

28

(2) INFORMATION FOR SEQ ID NO:15:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

60

61

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5 ATGGATCCTC GGACTCCATC TCTTCTTG

28

(2) INFORMATION FOR SEQ ID NO:16:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20 ATGGATCCTC AGGACTCCAT CTCTTCTTG

29

(2) INFORMATION FOR SEQ ID NO:17:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCTCGAGCC ATCATGAGCA GAAGCAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45 GTGGATCCCA CTGCTGCACC TGTGCTA

27

(2) INFORMATION FOR SEQ ID NO:19:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

61

GTGGATCCTC ACTGCTGCAC CTGTGCTA

28

(2) INFORMATION FOR SEQ ID NO:20:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15

CGCGAATTCC GCCACCATGA GTGCTGAGGG GTACCAGTAC

40

(2) INFORMATION FOR SEQ ID NO:21:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGGATCCT GTCGCCTCTG CTGTGCATAT AC

32

30

(2) INFORMATION FOR SEQ ID NO:22:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: p85-top-C

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGAGATCTA TGAGTGCTGA GGGGTACCAAG

30

45

(2) INFORMATION FOR SEQ ID NO:23:

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGC GGATCC TCATGCCCTC TGCTGTGCAT ATAC

34

62

(2) INFORMATION FOR SEQ ID NO:24:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGAATTCGA CCATGTCGTC CATCTTGCCA TTC

33

15

(2) INFORMATION FOR SEQ ID NO:25:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

25

GTGGTACCCA TGACATGCTT GAGCAACGCA C

31

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

40

GTGGTACCTT ATGACATGCT TGAGCAACGC AC

32

(2) INFORMATION FOR SEQ ID NO:27:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGAATTCTG CAATGGAGCT GGAAAACATC G

31

55

- (2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:

63

64

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGGATCCCT GCTGCTTCCG GTGGAGTTCG

30

10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGATCCCT AGCTGCTTCC GGTGGAGTTC G

31

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

35

GTAGATCTAC CATGGCGGGC TGGATCCAGG CC

32

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTGGTACCCA TGAGAGGGAG CCTCTGGCAG A

31

50

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 GTGGTACCTC ATGAGAGGGA GCCTCTGGCA G 31

(2) INFORMATION FOR SEQ ID NO:33:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGAATTCAA CCATGGACAA TATGTCTATT ACG 33

20 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

30 GTGGATCCCA GTCTAAAGGT TGTGGGTCTG C 31

(2) INFORMATION FOR SEQ ID NO:35:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTGGATCCTC AGTCTAAAGG TTGTGGGTCT GC 32

45 (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

66

GTCTCGAGGC ACCATGAGCG ACGTGGC

27

(2) INFORMATION FOR SEQ ID NO:37:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGATCCGA GGCGGTGCTG CTGGCCG

27

- 15 (2) INFORMATION FOR SEQ ID NO:38:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1896 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1891
 (D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
35 1 5 10 15	

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
40 20 25 30	

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
45 35 40 45	

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
55 65 70 75 80	

CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
55 85 90 95	

66

67

	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
20	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
25	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
30	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
35	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
40	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720
45	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCA ACC ATG GCG GCG GCG Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala 245 250 255	768
50	GCG GCT CAG GGG GGC GGG GGC GGG GAG CCC CGT AGA ACC GAG GGG GTC Ala Ala Gln Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val 260 265 270	816
55	GGC CCG GGG GTC CCG GGG GAG GTG GAG ATG GTG AAG GGG CAG CCG TTC Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe 275 280 285	864
55	GAC GTG GGC CCG CGC TAC ACG CAG TTG CAG TAC ATC GGC GAG GGC GCG Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala 290 295 300	912
55	TAC GGC ATG GTC AGC TCG GCC TAT GAC CAC GTG CGC AAG ACT CGC GTG Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val 305 310 315 320	960

68

	GCC ATC AAG AAG ATC AGC CCC TTC GAA CAT CAG ACC TAC TGC CAG CGC Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg 325 330 335	1008
5	ACG CTC CGG GAG ATC CAG ATC CTG CTG CGC TTC CGC CAT GAG AAT GTC Thr Leu Arg Glu Ile Gln Ile Leu Arg Phe Arg His Glu Asn Val 340 345 350	1056
10	ATC GGC ATC CGA GAC ATT CTG CGG GCG TCC ACC CTG GAA GCC ATG AGA Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg 355 360 365	1104
15	GAT GTC TAC ATT GTG CAG GAC CTG ATG GAG ACT GAC CTG TAC AAG TTG Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu 370 375 380	1152
20	CTG AAA AGC CAG CAG CTG AGC ATT GAC CAT ATC TGC TAC TTC CTC TAC Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr 385 390 395 400	1200
25	CAG ATC CTG CGG GGC CTC AAG TAC ATC CAC TCC GCC AAC GTG CTC CAC Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His 405 410 415	1248
30	CGA GAT CTA AAG CCC TCC AAC CTG CTC AGC AAC ACC ACC TGC GAC CTT Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu 420 425 430	1296
35	AAG ATT TGT GAT TTC GGC CTG GCC CGG ATT GCC GAT CCT GAG CAT GAC Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp 435 440 445	1344
40	CAC ACC GGC TTC CTG ACG GAG TAT GTG GCT ACG CGC TGG TAC CGG GCC His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala 450 455 460	1392
45	CCA GAG ATC ATG CTG AAC TCC AAG GGC TAT ACC AAG TCC ATC GAC ATC Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile 465 470 475 480	1440
50	TGG TCT GTG GGC TGC ATT CTG GCT GAG ATG CTC TCT AAC CGG CCC ATC Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile 485 490 495	1488
55	TTC CCT GGC AAG CAC TAC CTG GAT CAG CTC AAC CAC ATT CTG GGC ATC Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile 500 505 510	1536
50	CTG GGC TCC CCA TCC CAG GAG GAC CTG AAT TGT ATC ATC AAC ATG AAG Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys 515 520 525	1584
55	GCC CGA AAC TAC CTA CAG TCT CTG CCC TCC AAG ACC AAG GTG GCT TGG Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp 530 535 540	1632

69

	GCC AAG CTT TTC CCC AAG TCA GAC TCC AAA GCC CTT GAC CTG CTG GAC Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp 545 550 555 560	1680
5	CGG ATG TTA ACC TTT AAC CCC AAT AAA CGG ATC ACA GTG GAG GAA GCG Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala 565 570 575	1728
10	CTG GCT CAC CCC TAC CTG GAG CAG TAC TAT GAC CCG ACG GAT GAG CCA Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro 580 585 590	1776
15	GTG GCC GAG GAG CCC TTC ACC TTC GCC ATG GAG CTG GAT GAC CTA CCT Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro 595 600 605	1824
	AAG GAG CGG CTG AAG GAG CTC ATC TTC CAG GAG ACA GCA CGC TTC CAG Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln 610 615 620	1872
20	CCC GGA GTG CTG GAG GCC C CCTAG Pro Gly Val Leu Glu Ala Pro 625 630	1896

25

(2) INFORMATION FOR SEQ ID NO:39:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 631 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
35	(v) FRAGMENT TYPE: internal
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
40	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45 45 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 50 85 90 95 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125 55 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 5 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 10 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala
 245 250 255
 15 Ala Ala Gln Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val
 260 265 270
 Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe
 275 280 285
 Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala
 20 290 295 300
 Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val
 305 310 315 320
 Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg
 325 330 335
 25 Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu Asn Val
 340 345 350
 Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg
 355 360 365
 Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu
 30 370 375 380
 Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr
 385 390 395 400
 Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His
 405 410 415
 35 Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu
 420 425 430
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp
 435 440 445
 His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala
 40 450 455 460
 Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile
 465 470 475 480
 Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile
 485 490 495
 45 Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile
 500 505 510
 Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys
 515 520 525
 Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp
 50 530 535 540
 Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp
 545 550 555 560
 Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala
 565 570 575
 55 Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro
 580 585 590

71

	Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro		
	595	600	605
	Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln		
	610	615	620
5	Pro Gly Val Leu Glu Ala Pro		
	625	630	

(2) INFORMATION FOR SEQ ID NO:40:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA
(ix) FEATURE:20 (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1815
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

25	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
30	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
35	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
40	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
45	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
50	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
55	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384

72

	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
5	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
10	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
15	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
20	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
25	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
30	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720
35	GGA CTC AGA TCT CGA GTA ACC ATG GCG GCG GCG GCG GCG GCG GCG CCG Gly Leu Arg Ser Arg Val Thr Met Ala Ala Ala Ala Ala Gly Pro 245 250 255	768
40	GAG ATG GTC CGC GGG CAG GTG TTC GAC GTG GGG CCG CGC TAC ACT AAT Glu Met Val Arg Gly Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn 260 265 270	816
45	CTC TCG TAC ATC GGA GAA GGC GCC TAC GGC ATG GTT TGT TCT GCT TAT Leu Ser Tyr Ile Gly Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr 275 280 285	864
50	GAT AAT CTC AAC AAA GTT CGA GTT GCT ATC AAG AAA ATC AGT CCT TTT Asp Asn Leu Asn Lys Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe 290 295 300	912
55	GAG CAC CAG ACC TAC TGT CAG AGA ACC CTG AGA GAG ATA AAA ATC CTA Glu His Gln Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu 305 310 315 320	960
55	CTG CGC TTC AGA CAT GAG AAC ATC ATC GGC ATC AAT GAC ATC ATC CGG Leu Arg Phe Arg His Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg 325 330 335	1008
55	GCA CCA ACC ATT GAG CAG ATG AAA GAT GTA TAT ATA GTA CAG GAC CTC Ala Pro Thr Ile Glu Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu 340 345 350	1056

73

	ATG GAG ACA GAT CTT TAC AAG CTC TTG AAG ACA CAG CAC CTC AGC AAT Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn 355	360	365	1104
5	GAT CAT ATC TGC TAT TTT CTT TAT CAG ATC CTG AGA GGA TTA AAG TAT Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr 370	375	380	1152
10	ATA CAT TCA GCT AAT GTT CTG CAC CGT GAC CTC AAG CCT TCC AAC CTC Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu 385	390	395	400
15	CTG CTG AAC ACC ACT TGT GAT CTC AAG ATC TGT GAC TTT GGC CTT GCC Leu Leu Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala 405	410	415	1248
20	CGT GTT GCA GAT CCA GAC CAT GAT CAT ACA GGG TTC TTG ACA GAG TAT Arg Val Ala Asp Pro Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr 420	425	430	1296
25	GTA GCC ACG CGT TGG TAC AGA GCT CCA GAA ATT ATG TTG AAT TCC AAG Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys 435	440	445	1344
30	GGT TAT ACC AAG TCC ATT GAT ATT TGG TCT GTG GGC TGC ATC CTG GCA Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala 450	455	460	1392
35	GAG ATG CTA TCC AAC AGG CCT ATC TTC CCA GGA AAG CAT TAC CTT GAC Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp 465	470	475	1440
40	CAG CTG AAT CAC ATC CTG GGT ATT CTT GGA TCT CCA TCA CAG GAA GAT Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp 485	490	495	1488
45	CTG AAT TGT ATA ATA AAT TTA AAA GCT AGA AAC TAT TTG CTT TCT CTC Leu Asn Cys Ile Ile Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu 500	505	510	1536
50	CCG CAC AAA AAT AAG GTG CCG TGG AAC AGG TTG TTC CCA AAC GCT GAC Pro His Lys Asn Lys Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp 515	520	525	1584
55	TCC AAA GCT CTG GAT TTA CTG GAT AAA ATG TTG ACA TTT AAC CCT CAC Ser Lys Ala Leu Asp Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His 530	535	540	1632
60	AAG AGG ATT GAA GTT GAA CAG GCT CTG GCC CAC CCG TAC CTG GAG CAG Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln 545	550	555	1680
65	TAT TAT GAC CCA AGT GAT GAG CCC ATT GCT GAA GCA CCA TTC AAG TTT Tyr Tyr Asp Pro Ser Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe 565	570	575	1728

GAC ATG GAG CTG GAC GAC TTA CCT AAG GAG AAG CTC AAA GAA CTC ATT 1776
 Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile
 580 585 590

5 TTT GAA GAG ACT GCT CGA TTC CAG CCA GGA TAC AGA TCT TAA 1818
 Phe Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser
 595 600 605

10 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 amino acids
- (B) TYPE: amino acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 25 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 30 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 35 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 40 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 45 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 50 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Val Thr Met Ala Ala Ala Ala Ala Gly Pro
 245 250 255
 55 Glu Met Val Arg Gly Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn
 260 265 270

75

	Leu Ser Tyr Ile Gly Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr	
	275	280
	Asp Asn Leu Asn Lys Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe	
	290	295
5	Glu His Gln Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu	
	305	310
	Leu Arg Phe Arg His Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg	
	325	330
10	Ala Pro Thr Ile Glu Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu	
	340	345
	Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn	
	355	360
	Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr	
	370	375
15	Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu	
	385	390
	Leu Leu Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala	
	405	410
20	Arg Val Ala Asp Pro Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr	
	420	425
	Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys	
	435	440
	Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala	
	450	455
25	Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp	
	465	470
	Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp	
	485	490
30	Leu Asn Cys Ile Ile Asn Leu Lys Ala Arg Asn Tyr Leu Ser Leu	
	500	505
	Pro His Lys Asn Lys Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp	
	515	520
	Ser Lys Ala Leu Asp Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His	
	530	535
35	Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln	
	545	550
	Tyr Tyr Asp Pro Ser Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe	
	565	570
40	Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile	
	580	585
	Phe Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser	
	595	600
		605

(2) INFORMATION FOR SEQ ID NO:42:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 55 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2526

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

5	ATG GTG AGC AAG GGC GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
65	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624

77

	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
5	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720
10	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG TCA ATG GAG CTG GAA Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu 245 250 255	768
15	AAC ATC GTG GCC AAC ACG GTC TTG CTG AAA GCC AGG GAA GGG GGC GGA Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly 260 265 270	816
20	GGA AAG CGC AAA GGG AAA AGC AAG AAG TGG AAA GAA ATC CTG AAG TTC Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe 275 280 285	864
25	CCT CAC ATT AGC CAG TGT GAA GAC CTC CGA AGG ACC ATA GAC AGA GAT Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr Ile Asp Arg Asp 290 295 300	912
30	TAC TGC AGT TTA TGT GAC AAG CAG CCA ATC GGG AGG CTG CTT TTC CGG Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg Leu Leu Phe Arg 305 310 315 320	960
35	CAG TTT TGT GAA ACC AGG CCT GGG CTG GAG TGT TAC ATT CAG TTC CTG Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr Ile Gln Phe Leu 325 330 335	1008
40	GAC TCC GTG GCA GAA TAT GAA GTT ACT CCA GAT GAA AAA CTG GGA GAG Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu Lys Leu Gly Glu 340 345 350	1056
45	AAA GGG AAG GAA ATT ATG ACC AAG TAC CTC ACC CCA AAG TCC CCT GTT Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro Lys Ser Pro Val 355 360 365	1104
50	TTC ATA GCC CAA GTT GGC CAA GAC CTG GTC TCC CAG ACG GAG GAG AAG Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln Thr Glu Glu Lys 370 375 380	1152
55	CTC CTA CAG AAG CCG TGC AAA GAA CTC TTT TCT GCC TGT GCA CAG TCT Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala Cys Ala Gln Ser 385 390 395 400	1200
	GTC CAC GAG TAC CTG AGG GGA GAA CCA TTC CAC GAA TAT CTG GAC AGC Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu Tyr Leu Asp Ser 405 410 415	1248
	ATG TTT TTT GAC CGC TTT CTC CAG TGG AAG TGG TTG GAA AGG CAA CCG Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu Glu Arg Gln Pro 420 425 430	1296

	GTG ACC AAA AAC ACT TTC AGG CAG TAT CGA GTG CTA GGA AAA GGG GGC Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu Gly Lys Gly Gly 435 440 445	1344
5	TTC GGG GAG GTC TGT GCC TGC CAG GTT CGG GCC ACG GGT AAA ATG TAT Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr Gly Lys Met Tyr 450 455 460	1392
10	GCC TGC AAG CGC TTG GAG AAG AAG AGG ATC AAA AAG AGG AAA GGG GAG Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys Arg Lys Gly Glu 465 470 475 480	1440
15	TCC ATG GCC CTC AAT GAG AAG CAG ATC CTC GAG AAG GTC AAC AGT CAG Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys Val Asn Ser Gln 485 490 495	1488
20	TTT GTG GTC AAC CTG GCC TAT GCC TAC GAG ACC AAG GAT GCA CTG TGC Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys Asp Ala Leu Cys 500 505 510	1536
25	TTG GTC CTG ACC ATC ATG AAT GGG GGT GAC CTG AAG TTC CAC ATC TAC Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys Phe His Ile Tyr 515 520 525	1584
30	AAC ATG GGC AAC CCT GGC TTC GAG GAG GAG CGG GCC TTG TAT GCG Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala Leu Phe Tyr Ala 530 535 540	1632
35	GCA GAG ATC CTC TGC GGC TTA GAA GAC CTC CAC CGT GAG AAC ACC GTC Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg Glu Asn Thr Val 545 550 555 560	1680
40	TAC CGA GAT CTG AAA CCT GAA AAC ATC CTG TTA GAT GAT TAT GGC CAC Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Asp Tyr Gly His 565 570 575	1728
45	ATT AGG ATC TCA GAC CTG GGC TTG GCT GTG AAG ATC CCC GAG GGA GAC Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile Pro Glu Gly Asp 580 585 590	1776
50	CTG ATC CGC GGC CGG GTG GGC ACT GTT GGC TAC ATG GCC CCC GAA GTC Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met Ala Pro Glu Val 595 600 605	1824
55	CTG AAC AAC CAG AGG TAC GGC CTG AGC CCC GAC TAC TGG GGC CTT GGC Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr Trp Gly Leu Gly 610 615 620	1872
	TGC CTC ATC TAT GAG ATG ATC GAG GGC CAG TCG CCG TTC CGC GGC CGT Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro Phe Arg Gly Arg 625 630 635 640	1920
	AAG GAG AAG GTG AAG CGG GAG GAG GTG GAC CGC CGG GTC CTG GAG ACG Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg Val Leu Glu Thr 645 650 655	1968

79

	GAG GAG GTG TAC TCC CAC AAG TTC TCC GAG GAG GCC AAG TCC ATC TGC Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala Lys Ser Ile Cys 660 665 670	2016
5	AAG ATG CTG CTC ACG AAA GAT GCG AAG CAG AGG CTG GGC TGC CAG GAG Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu Gly Cys Gln Glu 675 680 685	2064
10	GAG GGG GCT GCA GAG GTC AAG AGA CAC CCC TTC TTC AGG AAC ATG AAC Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe Arg Asn Met Asn 690 695 700	2112
15	TTC AAG CGC TTA GAA GCC GGG ATG TTG GAC CCT CCC TTC GTT CCA GAC Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro Phe Val Pro Asp 705 710 715 720	2160
20	CCC CGC GCT GTG TAC TGT AAG GAC GTG CTG GAC ATC GAG CAG TTC TCC Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile Glu Gln Phe Ser 725 730 735	2208
25	ACT GTG AAG GGC GTC AAT CTG GAC CAC ACA GAC GAC GAC TTC TAC TCC Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp Asp Phe Tyr Ser 740 745 750	2256
30	AAG TTC TCC ACG GGC TCT GTG TCC ATC CCA TGG CAA AAC GAG ATG ATA Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln Asn Glu Met Ile 755 760 765	2304
35	GAA ACA GAA TGC TTT AAG GAG CTG AAC GTG TTT GGA CCT AAT GGT ACC Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly Pro Asn Gly Thr 770 775 780	2352
40	CTC CCG CCA GAT CTG AAC AGA AAC CAC CCT CCG GAA CCC AAG AAA Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu Pro Pro Lys Lys 785 790 795 800	2400
45	GGG CTG CTC CAG AGA CTC TTC AAG CGG CAG CAT CAG AAC AAT TCC AAG Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln Asn Asn Ser Lys 805 810 815	2448
50	AGT TCG CCC AGC TCC AAG ACC AGT TTT AAC CAC CAC ATA AAC TCA AAC Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His Ile Asn Ser Asn 820 825 830	2496
55	CAT GTC AGC TCG AAC TCC ACC GGA AGC AGC TAG His Val Ser Ser Asn Ser Thr Gly Ser Ser 835 840	2529

50 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
10	20	25	30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	35	40	45	
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
	50	55	60	
15	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
	65	70	75	80
	Gln His Asp Phe Phe Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
	85	90	95	
20	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
	100	105	110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
	115	120	125	
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
	130	135	140	
25	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
	145	150	155	160
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
	165	170	175	
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
30	180	185	190	
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
	195	200	205	
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
	210	215	220	
35	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
	225	230	235	240
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu			
	245	250	255	
	Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly			
40	260	265	270	
	Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe			
	275	280	285	
	Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr Ile Asp Arg Asp			
	290	295	300	
45	Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg Leu Leu Phe Arg			
	305	310	315	320
	Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr Ile Gln Phe Leu			
	325	330	335	
	Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu Lys Leu Gly Glu			
50	340	345	350	
	Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro Lys Ser Pro Val			
	355	360	365	
	Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln Thr Glu Glu Lys			
	370	375	380	
55	Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala Cys Ala Gln Ser			
	385	390	395	400

Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu Tyr Leu Asp Ser
 405 410 415
 Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu Glu Arg Gln Pro
 420 425 430
 5 Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu Gly Lys Gly Gly
 435 440 445
 Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr Gly Lys Met Tyr
 450 455 460
 Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys Arg Lys Gly Glu
 10 465 470 475 480
 Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys Val Asn Ser Gln
 485 490 495
 Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys Asp Ala Leu Cys
 500 505 510
 15 Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys Phe His Ile Tyr
 515 520 525
 Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala Leu Phe Tyr Ala
 530 535 540
 Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg Glu Asn Thr Val
 20 545 550 555 560
 Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Asp Tyr Gly His
 565 570 575
 Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile Pro Glu Gly Asp
 580 585 590
 25 Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met Ala Pro Glu Val
 595 600 605
 Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr Trp Gly Leu Gly
 610 615 620
 Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro Phe Arg Gly Arg
 30 625 630 635 640
 Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg Val Leu Glu Thr
 645 650 655
 Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala Lys Ser Ile Cys
 660 665 670
 35 Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu Gly Cys Gln Glu
 675 680 685
 Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe Arg Asn Met Asn
 690 695 700
 Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro Phe Val Pro Asp
 40 705 710 715 720
 Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile Glu Gln Phe Ser
 725 730 735
 Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp Asp Phe Tyr Ser
 740 745 750
 45 Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln Asn Glu Met Ile
 755 760 765
 Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly Pro Asn Gly Thr
 770 775 780
 Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu Pro Pro Lys Lys
 50 785 790 795 800
 Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln Asn Asn Ser Lys
 805 810 815
 Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His Ile Asn Ser Asn
 820 825 830
 55 His Val Ser Ser Asn Ser Thr Gly Ser Ser
 835 840

(2) INFORMATION FOR SEQ ID NO:44:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1902 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1899
- (D) OTHER INFORMATION:

15 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

20	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
60	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
65	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480

83

	145	150	155	160	
5	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser				528
	165	170		175	
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly				576
	180	185		190	
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu				624
	195	200		205	
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe				672
	210	215		220	
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser				720
	225	230		235	
	240				
30	GGA CTC AGA TCT CGA GCT CGA GCC ATC ATG AGC AGA AGC AAG CGT GAC Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp				768
	245	250		255	
35	AAC AAT TTT TAT AGT GTA GAG ATT GGA GAT TCT ACA TTC ACA GTC CTG Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu				816
	260	265		270	
40	AAA CGA TAT CAG AAT TTA AAA CCT ATA GGC TCA GGA GCT CAA GGA ATA Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile				864
	275	280		285	
45	GTA TGC GCA GCT TAT GAT GCC ATT CTT GAA AGA AAT GTT GCA ATC AAG Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys				912
	290	295		300	
50	AAG CTA AGC CGA CCA TTT CAG AAT CAG ACT CAT GCC AAG CGG GCC TAC Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr				960
	305	310		315	
	320				
55	AGA GAG CTA GTT CTT ATG AAA TGT GTT AAT CAC AAA AAT ATA ATT GGC Arg Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Gly				1008
	325	330		335	
	340	345		350	
55	CTT TTG AAT GTT TTC ACA CCA CAG AAA TCC CTA GAA GAA TTT CAA GAT Leu Leu Asn Val Phe Thr Pro Gln Lys Ser Leu Glu Glu Phe Gln Asp				1056
	355	360		365	
	370				
55	GTT TAC ATA GTC ATG GAG CTC ATG GAT GCA AAT CTT TGC CAA GTG ATT Val Tyr Ile Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile				1104
	375	380		385	
	390				
55	CAG ATG GAG CTA GAT CAT GAA AGA ATG TCC TAC CTT CTC TAT CAG ATG Gln Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met				1152

84

	370	375	380	
5	CTG TGT GGA ATC AAG CAC CTT CAT TCT GCT GGA ATT ATT CAT CGG GAC Leu Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp 385 390 395 400			1200
10	TTA AAG CCC AGT AAT ATA GTA GTA AAA TCT GAT TGC ACT TTG AAG ATT Leu Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile 405 410 415			1248
15	CTT GAC TTC GGT CTG GCC AGG ACT GCA GGA ACG AGT TTT ATG ATG ACG Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr 420 425 430			1296
20	CCT TAT GTA GTG ACT CGC TAC TAC AGA GCA CCC GAG GTC ATC CTT GGC Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly 435 440 445			1344
25	ATG GGC TAC AAG GAA AAC GTG GAT TTA TGG TCT GTG GGG TGC ATT ATG Met Gly Tyr Lys Glu Asn Val Asp Leu Trp Ser Val Gly Cys Ile Met 450 455 460			1392
30	GGA GAA ATG GTT TGC CAC AAA ATC CTC TTT CCA GGA AGG GAC TAT ATT Gly Glu Met Val Cys His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile 465 470 475 480			1440
35	GAT CAG TGG AAT AAA GTT ATT GAA CAG CTT GGA ACA CCA TGT CCT GAA Asp Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu 485 490 495			1488
40	TTC ATG AAG AAA CTG CAA CCA ACA GTC AGG ACT TAC GTT GAA AAC AGA Phe Met Lys Lys Leu Gln Pro Thr Val Arg Thr Tyr Val Glu Asn Arg 500 505 510			1536
45	CCT AAA TAT GCT GGA TAT AGC TTT GAG AAA CTC TTC CCT GAT GTC CTT Pro Lys Tyr Ala Gly Tyr Ser Phe Glu Lys Leu Phe Pro Asp Val Leu 515 520 525			1584
50	TTC CCA GCT GAC TCA GAA CAC AAC AAA CTT AAA GCC AGT CAG GCA AGG Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg 530 535 540			1632
55	GAT TTG TTA TCC AAA ATG CTG GTA ATA GAT GCA TCT AAA AGG ATC TCT Asp Leu Leu Ser Lys Met Leu Val Ile Asp Ala Ser Lys Arg Ile Ser 545 550 555 560			1680
60	GTA GAT GAA GCT CTC CAA CAC CCG TAC ATC AAT GTC TGG TAT GAT CCT Val Asp Glu Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro 565 570 575			1728
65	TCT GAA GCA GAA GCT CCA CCA AAG ATC CCT GAC AAG CAG TTA GAT Ser Glu Ala Glu Ala Pro Pro Lys Ile Pro Asp Lys Gln Leu Asp 580 585 590			1776
70	GAA AGG GAA CAC ACA ATA GAA GAG TGG AAA GAA TTG ATA TAT AAG GAA Glu Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu			1824

85

595 600 605

5 GTT ATG GAC TTG GAG GAG AGA ACC AAG AAT GGA GTT ATA CGG GGG CAG 1872
 Val Met Asp Leu Glu Glu Arg Thr Lys Asn Gly Val Ile Arg Gly Gln
 610 615 620

10 CCC TCT CCT TTA GCA CAG GTG CAG CAG TGA 1902
 Pro Ser Pro Leu Ala Gln Val Gln Gln
 625 630

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 633 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

25 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 30 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 35 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 40 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 45 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 50 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 55 Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp
 245 250 255

86

50 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1824 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sin

55 (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 5 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1821
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

10	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
15	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
20	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
25	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
30	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
35	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
40	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
45	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
50	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
55	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
60	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
65	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	576

88

	180	185	190	
	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			624
5	195	200	205	
	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			672
	210	215	220	
10	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			720
	225	230	235	240
15	GGA CTC AGA TCT CGA GGG AAA ATG TCT CAG GAG AGG CCC ACG TTC TAC Gly Leu Arg Ser Arg Gly Lys Met Ser Gln Glu Arg Pro Thr Phe Tyr			768
	245	250	255	
20	CGG CAG GAG CTG AAC AAG ACA ATC TGG GAG GTG CCC GAG CGT TAC CAG Arg Gln Glu Leu Asn Lys Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln			816
	260	265	270	
25	AAC CTG TCT CCA GTG GGC TCT GGC GCC TAT GGC TCT GTG TGT GCT GCT Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala			864
	275	280	285	
	TTT GAC ACA AAA ACG GGG TTA CGT GTG GCA GTG AAG AAG CTC TCC AGA Phe Asp Thr Lys Thr Gly Leu Arg Val Ala Val Lys Lys Leu Ser Arg			912
	290	295	300	
30	CCA TTT CAG TCC ATC ATT CAT GCG AAA AGA ACC TAC AGA GAA CTG CGG Pro Phe Gln Ser Ile Ile His Ala Lys Arg Thr Tyr Arg Glu Leu Arg			960
	305	310	315	320
35	TTA CTT AAA CAT ATG AAA CAT GAA AAT GTG ATT GGT CTG TTG GAC GTT Leu Leu Lys His Met Lys His Glu Asn Val Ile Gly Leu Leu Asp Val			1008
	325	330	335	
40	TTT ACA CCT GCA AGG TCT CTG GAG GAA TTC AAT GAT GTG TAT CTG GTG Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe Asn Asp Val Tyr Leu Val			1056
	340	345	350	
	ACC CAT CTC ATG GGG GCA GAT CTG AAC AAC ATT GTG AAA TGT CAG AAG Thr His Leu Met Gly Ala Asp Leu Asn Asn Ile Val Lys Cys Gln Lys			1104
45	355	360	365	
	CTT ACA GAT GAC CAT GTT CAG TTC CTT ATC TAC CAA ATT CTC CGA GGT Leu Thr Asp Asp His Val Gln Phe Leu Ile Tyr Gln Ile Leu Arg Gly			1152
	370	375	380	
50	CTA AAG TAT ATA CAT TCA GCT GAC ATA ATT CAC AGG GAC CTA AAA CCT Leu Lys Tyr Ile His Ser Ala Asp Ile Ile His Arg Asp Leu Lys Pro			1200
	385	390	395	400
55	AGT AAT CTA GCT GTG AAT GAA GAC TGT GAG CTG AAG ATT CTG GAT TTT Ser Asn Leu Ala Val Asn Glu Asp Cys Glu Leu Lys Ile Leu Asp Phe			1248

	405	410	415	
5	GGA CTG GCT CGG CAC ACA GAT GAT GAA ATG ACA GGC TAC GTG GCC ACT Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val Ala Thr 420	425	430	1296
10	AGG TGG TAC AGG GCT CCT GAG ATC ATG CTG AAC TGG ATG CAT TAC AAC Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His Tyr Asn 435	440	445	1344
15	CAG ACA GTT GAT ATT TGG TCA GTG GGA TGC ATA ATG GCC GAG CTG TTG Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu Leu Leu 450	455	460	1392
20	ACT GGA AGA ACA TTG TTT CCT GGT ACA GAC CAT ATT GAT CAG TTG AAG Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln Leu Lys 465	470	475	1440
25	CTC ATT TTA AGA CTC GTT GGA ACC CCA GGG GCT GAG CTT TTG AAG AAA Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu Lys Lys 485	490	495	1488
30	ATC TCC TCA GAG TCT GCA AGA AAC TAT ATT CAG TCT TTG ACT CAG ATG Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr Gln Met 500	505	510	1536
35	CCG AAG ATG AAC TTT GCG AAT GTA TTT ATT GGT GCC AAT CCC CTG GCT Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro Leu Ala 515	520	525	1584
40	GTC GAC TTG CTG GAG AAG ATG CTT GTA TTG GAC TCA GAT AAG AGA ATT Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys Arg Ile 530	535	540	1632
45	ACA GCG GCC CAA GCC CTT GCA CAT GCC TAC TTT GCT CAG TAC CAC GAT Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr His Asp 545	550	555	1680
50	CCT GAT GAT GAA CCA GTG GCC GAT CCT TAT GAT CAG TCC TTT GAA AGC Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe Glu Ser 565	570	575	1728
55	AGG GAC CTC CTT ATA GAT GAG TGG AAA AGC CTG ACC TAT GAT GAA GTC Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp Glu Val 580	585	590	1776
60	ATC AGC TTT GTG CCA CCA CCC CTT GAC CAA GAA GAG ATG GAG TCC TGA Ile Ser Phe Val Pro Pro Leu Asp Gln Glu Glu Met Glu Ser 595	600	605	1824

(2) INFORMATION FOR SEQ ID NO:47:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 607 amino acids
(B) TYPE: amino acid

90

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

10	Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
15	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
30	165 170 175	
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
35	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
	Gly Leu Arg Ser Arg Gly Lys Met Ser Gln Glu Arg Pro Thr Phe Tyr	
40	245 250 255	
	Arg Gln Glu Leu Asn Lys Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln	
	260 265 270	
	Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala	
	275 280 285	
45	Phe Asp Thr Lys Thr Gly Leu Arg Val Ala Val Lys Lys Leu Ser Arg	
	290 295 300	
	Pro Phe Gln Ser Ile Ile His Ala Lys Arg Thr Tyr Arg Glu Leu Arg	
	305 310 315 320	
	Leu Leu Lys His Met Lys His Glu Asn Val Ile Gly Leu Leu Asp Val	
50	325 330 335	
	Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe Asn Asp Val Tyr Leu Val	
	340 345 350	
	Thr His Leu Met Gly Ala Asp Leu Asn Asn Ile Val Lys Cys Gln Lys	
	355 360 365	
55	Leu Thr Asp Asp His Val Gln Phe Leu Ile Tyr Gln Ile Leu Arg Gly	
	370 375 380	

90

91

Leu Lys Tyr Ile His Ser Ala Asp Ile Ile His Arg Asp Leu Lys Pro
 385 390 395 400
 Ser Asn Leu Ala Val Asn Glu Asp Cys Glu Leu Lys Ile Leu Asp Phe
 405 410 415
 5 Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val Ala Thr
 420 425 430
 Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His Tyr Asn
 435 440 445
 10 Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu Leu Leu
 450 455 460
 Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln Leu Lys
 465 470 475 480
 Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu Lys Lys
 485 490 495
 15 Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr Gln Met
 500 505 510
 Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro Leu Ala
 515 520 525
 Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys Arg Ile
 20 530 535 540
 Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr His Asp
 545 550 555 560
 Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe Glu Ser
 565 570 575
 25 Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp Glu Val
 580 585 590
 Ile Ser Phe Val Pro Pro Leu Asp Gln Glu Glu Met Glu Ser
 595 600 605

30 (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2904
 - (D) OTHER INFORMATION:

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
50 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
55 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	

91

92

	35	40	45	
	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			192
5	50	55	60	
	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			240
	65	70	75	80
10	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			288
	85	90	95	
15	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			336
	100	105	110	
20	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			384
	115	120	125	
25	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			432
	130	135	140	
	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			480
	145	150	155	160
30	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			528
	165	170	175	
35	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			576
	180	185	190	
40	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			624
	195	200	205	
45	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			672
	210	215	220	
	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			720
	225	230	235	240
50	GGA CTC AGA TCT ATG AGT GCT GAG GGG TAC CAG TAC AGA GCG CTG TAT Gly Leu Arg Ser Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr			768
	245	250	255	
55	GAT TAT AAA AAG GAA AGA GAA GAT ATT GAC TTG CAC TTG GGT GAC Asp Tyr Lys Lys Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp			816

92

		93		
		260	265	270
5	ATA TTG ACT GTG AAT AAA GGG TCC TTA GTA GCT CTT GGA TTC AGT GAT Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp 275 280 285			864
10	GGA CAG GAA GCC AGG CCT GAA GAA ATT GGC TGG TTA AAT GGC TAT AAT Gly Gln Glu Ala Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn 290 295 300			912
15	GAA ACC ACA GGG GAA AGG GGG GAC TTT CCG GGA ACT TAC GTA GAA TAT Glu Thr Thr Gly Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr 305 310 315 320			960
20	ATT GGA AGG AAA AAA ATC TCG CCT CCC ACA CCA AAG CCC CGG CCA CCT Ile Gly Arg Lys Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro 325 330 335			1008
25	CGG CCT CTT CCT GTT GCA CCA GGT TCT TCG AAA ACT GAA GCA GAT GTT Arg Pro Leu Pro Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val 340 345 350			1056
30	GAA CAA CAA GCT TTG ACT CTC CCG GAT CTT GCA GAG CAG TTT GCC CCT Glu Gln Gln Ala Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro 355 360 365			1104
35	CCT GAC ATT GCC CCG CCT CTT CTT ATC AAG CTC GTG GAA GCC ATT GAA Pro Asp Ile Ala Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu 370 375 380			1152
40	AAG AAA GGT CTG GAA TGT TCA ACT CTA TAC AGA ACA CAG AGC TCC AGC Lys Lys Gly Leu Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser 385 390 395 400			1200
45	AAC CTG GCA GAA TTA CGA CAG CTT CTT GAT TGT GAT ACA CCC TCC GTG Asn Leu Ala Glu Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val 405 410 415			1248
50	GAC TTG GAA ATG ATC GAT GTG CAC GTT TTG GCT GAC GCT TTC AAA CGC Asp Leu Glu Met Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg 420 425 430			1296
55	TAT CTC CTG GAC TTA CCA AAT CCT GTC ATT CCA GCA GCC GTT TAC AGT Tyr Leu Leu Asp Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser 435 440 445			1344
55	GAA ATG ATT TCT TTA GCT CCA GAA GTA CAA AGC TCC GAA GAA TAT ATT Glu Met Ile Ser Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile 450 455 460			1392
55	CAG CTA TTG AAG AAG CTT ATT AGG TCG CCT AGC ATA CCT CAT CAG TAT Gln Leu Leu Lys Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr 465 470 475 480			1440
55	TGG CTT ACG CTT CAG TAT TTG TTA AAA CAT TTC TTC AAG CTC TCT CAA Trp Leu Thr Leu Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln			1498

	94	485	490	495	
5					
	ACC TCC AGC AAA AAT CTG TTG AAT GCA AGA GTA CTC TCT GAA ATT TTC Thr Ser Ser Lys Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe				1536
	500		505		510
10					
	AGC CCT ATG CTT TTC AGA TTC TCA GCA GCC AGC TCT GAT AAT ACT GAA Ser Pro Met Leu Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu				1584
	515		520		525
15					
	AAC CTC ATA AAA GTT ATA GAA ATT TTA ATC TCA ACT GAA TGG AAT GAA Asn Leu Ile Lys Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu				1612
	530		535		540
20					
	CGA CAG CCT GCA CCA GCA CTG CCT CCT AAA CCA CCA AAA CCT ACT ACT Arg Gln Pro Ala Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr				1680
	545		550		555
25					
	GTA GCC AAC AAC GGT ATG AAT AAC AAT ATG TCC TTA CAA AAT GCT GAA Val Ala Asn Asn Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu				1728
	565		570		575
30					
	TGG TAC TGG GGA GAT ATC TCG AGG GAA GAA GTG AAT GAA AAA CTT CGA Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg				1776
	580		585		590
35					
	GAT ACA GCA GAC GGG ACC TTT TTG GTA CGA GAT GCG TCT ACT AAA ATG Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met				1824
	595		600		605
40					
	CAT GGT GAT TAT ACT CTT ACA CTA AGG AAA GGG GGA AAT AAC AAA TTA His Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu				1872
	610		615		620
45					
	ATC AAA ATA TTT CAT CGA GAT GGG AAA TAT GGC TTC TCT GAC CCA TTA Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu				1920
	625		630		635
50					
	ACC TTC AGT TCT GTG GTT GAA TTA ATA AAC CAC TAC CGG AAT GAA TCT Thr Phe Ser Ser Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser				1968
	645		650		655
55					
	CTA GCT CAG TAT AAT CCC AAA TTG GAT GTG AAA TTA CTT TAT CCA GTA Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val				2016
	660		665		670
	675		680		685
	690		695		700
	705		710		715
	720		725		730
	735		740		745
	750		755		760
	765		770		775
	780		785		790
	795		800		805
	810		815		820
	825		830		835
	840		845		850
	855		860		865
	870		875		880
	885		890		895
	900		905		910
	915		920		925
	930		935		940
	945		950		955
	960		965		970
	975		980		985
	990		995		1000

		95		
	705	710	715	720
5	ATC CAA ATG AAA AGG ACA GCA ATT GAA GCA TTT AAT GAA ACC ATA AAA Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys 725 730 735			2208
10	ATA TTT GAA GAA CAG TGC CAG ACC CAA GAG CGG TAC AGC AAA GAA TAC Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr 740 745 750			2256
15	ATA GAA AAG TTT AAA CGT GAA GGC AAT GAG AAA GAA ATA CAA AGG ATT Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile 755 760 765			2304
20	ATG CAT AAT TAT GAT AAG TTG AAG TCT CGA ATC AGT GAA ATT ATT GAC Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp 770 775 780			2352
25	AGT AGA AGA AGA TTG GAA GAC TTG AAG AAG CAG GCA GCT GAG TAT Ser Arg Arg Arg Leu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr 785 790 795 800			2400
30	CGA GAA ATT GAC AAA CGT ATG AAC AGC ATT AAA CCA GAC CTT ATC CAG Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln 805 810 815			2448
35	CTG AGA AAG ACG AGA GAC CAA TAC TTG ATG TGG TTG ACT CAA AAA GGT Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly 820 825 830			2496
40	GTT CGG CAA AAG AAG TTG AAC GAG TGG TTG GGC AAT GAA AAC ACT GAA Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn Asn Thr Glu 835 840 845			2544
45	GAC CAA TAT TCA CTG GTG GAA GAT GAT GAA GAT TTG CCC CAT CAT GAT Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp 850 855 860			2592
50	GAG AAG ACA TGG AAT GTT GGA AGC AGC AAC CGA AAC AAA GCT GAA AAC Glu Lys Thr Trp Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn 865 870 875 880			2640
55	CTG TTG CGA GGG AAG CGA GAT GGC ACT TTT CTT GTC CGG GAG AGC AGT Leu Leu Arg Gly Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser 885 890 895			2688
	AAA CAG GGC TGC TAT GCC TGC TCT GTA GTG GTG GAC GGC GAA GTA AAG Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys 900 905 910			2736
	CAT TGT GTC ATA AAC AAA ACA GCA ACT GGC TAT GGC TTT GCC GAG CCC His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro 915 920 925			2784
	TAT AAC TTG TAC AGC TCT CTG AAA GAA CTG GTG CTA CAT TAC CAA CAC Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His			2832

	96		
	930	935	940
5	ACC TCC CTT GTG CAG CAC AAC GAC TCC CTC AAT GTC ACA CTA GCC TAC Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr		2880
	945	950	955
10	CCA GTA TAT GCA CAG CAG AGG CGA TGA Pro Val Tyr Ala Gln Gln Arg Arg 965		2907
	(2) INFORMATION FOR SEQ ID NO:49:		
15	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 968 amino acids		
	(B) TYPE: amino acid		
	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
20	(ii) MOLECULE TYPE: protein		
	(v) FRAGMENT TYPE: internal		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:		
25	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15		
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30		
30	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45		
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60		
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80		
35	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95		
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110		
40	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125		
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140		
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160		
45	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175		
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190		
50	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205		
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220		
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240		
55	Gly Leu Arg Ser Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr 245 250 255		

Asp Tyr Lys Lys Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp
 260 265 270
 Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp
 275 280 285
 5 Gly Gln Glu Ala Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn
 290 295 300
 Glu Thr Thr Gly Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr
 305 310 315 320
 Ile Gly Arg Lys Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro
 10 325 330 335
 Arg Pro Leu Pro Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val
 340 345 350
 Glu Gln Gln Ala Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro
 355 360 365
 15 Pro Asp Ile Ala Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu
 370 375 380
 Lys Lys Gly Leu Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser
 385 390 395 400
 Asn Leu Ala Glu Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val
 20 405 410 415
 Asp Leu Glu Met Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg
 420 425 430
 Tyr Leu Leu Asp Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser
 435 440 445
 25 Glu Met Ile Ser Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile
 450 455 460
 Gln Leu Leu Lys Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr
 465 470 475 480
 Trp Leu Thr Leu Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln
 30 485 490 495
 Thr Ser Ser Lys Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe
 500 505 510
 Ser Pro Met Leu Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu
 515 520 525
 35 Asn Leu Ile Lys Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu
 530 535 540
 Arg Gln Pro Ala Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr
 545 550 555 560
 Val Ala Asn Asn Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu
 40 565 570 575
 Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg
 580 585 590
 Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met
 595 600 605
 45 His Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu
 610 615 620
 Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu
 625 630 635 640
 Thr Phe Ser Ser Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser
 50 645 650 655
 Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val
 660 665 670
 Ser Lys Tyr Gln Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala
 675 680 685
 55 Val Gly Lys Lys Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser
 690 695 700

98

Arg Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu
 705 710 715 720
 Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys
 725 730 735
 5 Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr
 740 745 750
 Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile
 755 760 765
 Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp
 10 770 775 780
 Ser Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr
 785 790 795 800
 Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln
 805 810 815
 15 Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly
 820 825 830
 Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu
 835 840 845
 20 Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp
 850 855 860
 Glu Lys Thr Trp Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn
 865 870 875 880
 Leu Leu Arg Gly Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser
 885 890 895
 25 Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys
 900 905 910
 His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro
 915 920 925
 Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His
 30 930 935 940
 Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr
 945 950 955 960
 Pro Val Tyr Ala Gln Gln Arg Arg
 965

35

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2157
 - (D) OTHER INFORMATION:

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG
 Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 55 1 5 10 15

48

98

	99	
	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
5	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
10	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
15	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
20	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
25	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
30	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
35	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
40	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
45	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
50	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
55	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720

		100		
	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG ACC ATG TCG TCC ATC Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ser Ser Ile 245	250		255
5	TTG CCA TTC ACG CCG CCA GTT GTG AAG AGA CTG CTG GGA TGG AAG AAG Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys 260	265		270
10	TCA GCT GGT GGG TCT GGA GGA GCA GGC GGA GGA GAG CAG AAT GGG CAG Ser Ala Gly Gly Ser Gly Ala Gly Gly Glu Gln Asn Gly Gln 275	280		285
15	GAA GAA AAG TGG TGT GAG AAA GCA GTG AAA AGT CTG GTG AAG AAG CTA Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu 290	295		300
20	AAG AAA ACA GGA CGA TTA GAT GAG CTT GAG AAA GCC ATC ACC ACT CAA Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln 305	310		315
25	AAC TGT AAT ACT AAA TGT GTT ACC ATA CCA AGC ACT TGC TCT GAA ATT Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile 325	330		335
30	TGG GGA CTG AGT ACA CCA AAT ACG ATA GAT CAG TGG GAT ACA ACA GGC Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly 340	345		350
35	CTT TAC AGC TTC TCT GAA CAA ACC AGG TCT CTT GAT GGT CGT CTC CAG Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln 355	360		365
40	GTA TCC CAT CGA AAA GGA TTG CCA CAT GTT ATA TAT TGC CGA TTA TGG Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp 370	375		380
45	CGC TGG CCT GAT CTT CAC AGT CAT CAT GAA CTC AAG GCA ATT GAA AAC Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn 385	390		395
50	TGC GAA TAT GCT TTT AAT CTT AAA AAG GAT GAA GTA TGT GTA AAC CCT Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro 405	410		415
55	TAC CAC TAT CAG AGA GTT GAG ACA CCA GTT TTG CCT CCA GTC TTA GTG Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val 420	425		430
60	CCC CGA CAC ACC GAG ATC CTA ACA GAA CTT CCG CCT CTG GAT GAC TAT Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr 435	440		445
65	ACT CAC TCC ATT CCA GAA AAC ACT AAC TTC CCA GCA GGA ATT GAG CCA Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro 450	455		460

101

	CAG AGT AAT TAT ATT CCA GAA ACG CCA CCT GGA TAT ATC AGT GAA Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Gly Tyr Ile Ser Glu 465 470 475 480	1440
5	GAT GGA GAA ACA ACT GAC CAA CAG TTG AAT CAA AGT ATG GAC ACA GGC Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly 485 490 495	1488
10	TCT CCA GCA GAA CTA TCT CCT ACT ACT CTT TCC CCT GTT AAT CAT AGC Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser 500 505 510	1536
15	TTG GAT TTA CAG CCA GTT ACT TAC TCA GAA CCT GCA TTT TGG TGT TCA Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser 515 520 525	1584
20	ATA GCA TAT TAT GAA TTA AAT CAG AGG GTT GGA GAA ACC TTC CAT GCA Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala 530 535 540	1632
25	TCA CAG CCC TCA CTC ACT GTA GAT GGC TTT ACA GAC CCA TCA AAT TCA Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser 545 550 555 560	1680
30	GAG AGG TTC TGC TTA GGT TTA CTC TCC AAT GTT AAC CGA AAT GCC ACG Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr 565 570 575	1728
35	GTA GAA ATG ACA AGA AGG CAT ATA GGA AGA GGA GTG CGC TTA TAC TAC Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr 580 585 590	1776
40	ATA GGT GGG GAA GTT TTT GCT GAG TGC CTA AGT GAT AGT GCA ATC TTT Ile Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe 595 600 605	1824
45	GTG CAG AGC CCC AAT TGT AAT CAG AGA TAT GGC TGG CAC CCT GCA ACA Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr 610 615 620	1872
50	GTG TGT AAA ATT CCA CCA GGC TGT AAT CTG AAG ATC TTC AAC AAC CAG Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln 625 630 635 640	1920
55	GAA TTT GCT GCT CTT CTG GCT CAG TCT GTT AAT CAG GGT TTT GAA GCC Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala 645 650 655	1968
60	GTC TAT CAG CTA ACT AGA ATG TGC ACC ATA AGA ATG AGT TTT GTG AAA Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys 660 665 670	2016
65	GGG TGG GGA GCA GAA TAC CGA AGG CAG ACG GTA ACA AGT ACT CCT TGC Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys 675 680 685	2064

101

102

TGG ATT GAA CTT CAT CTG AAT GGA CCT CTA CAG TGG TTG GAC AAA GTA 2112
Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val
690 695 700

5 TTA ACT CAG ATG GGA TCC CCT TCA GTG CGT TGC TCA AGC ATG TCA TAA 2160
 Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
 705 710 715

10 (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: sin

(ii) MOLECULE TYPE: protein

(ii) MOLECULE TYPE: protein
(iv) FRAGMENTS TYPE: internal

20 (v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10				15		
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
						20			25				30		
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
								35	40			45			
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
						50		55			60				
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
						65		70		75				80	
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
							85			90			95		
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
						100			105				110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
						115			120			125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
						130		135			140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
						145		150			155			160	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
						165			170			175			
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
						180			185			190			
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
						195			200			205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Lys	Glu	Phe
						210		215			220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
						225		230			235			240	
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Ser	Ser	Ile
							245			250			255		
Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu	Gly	Trp	Lys	Lys
						260			265			270			

103

Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Glu Gln Asn Gly Gln
 275 280 285
 Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu
 290 295 300
 5 Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln
 305 310 315 320
 Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile
 325 330 335
 Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly
 10 340 345 350
 Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln
 355 360 365
 Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp
 370 375 380
 15 Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn
 385 390 395 400
 Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro
 405 410 415
 Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val
 20 420 425 430
 Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr
 435 440 445
 Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro
 450 455 460
 25 Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu
 465 470 475 480
 Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly
 485 490 495
 Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser
 30 500 505 510
 Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser
 515 520 525
 Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala
 530 535 540
 35 Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser
 545 550 555 560
 Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr
 565 570 575
 Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr
 40 580 585 590
 Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe
 595 600 605
 Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr
 610 615 620
 45 Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln
 625 630 635 640
 Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala
 645 650 655
 Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys
 50 660 665 670
 Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys
 675 680 685
 Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val
 690 695 700
 55 Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
 705 710 715

103

(2) INFORMATION FOR SEQ ID NO:52:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2421 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2418

15 (D) OTHER INFORMATION:
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

20	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
60	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
65	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480

		105		
	145	150	155	160
5	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			528
	165	170		175
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			576
	180	185		190
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			624
	195	200		205
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			672
	210	215		220
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			720
	225	230	235	240
30	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG AAT TCA ACC ATG GAC Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Asn Ser Thr Met Asp			768
	245	250		255
35	AAT ATG TCT ATT ACG AAT ACA CCA ACA AGT AAT GAT GCC TGT CTG AGC Asn Met Ser Ile Thr Asn Thr Pro Thr Ser Asn Asp Ala Cys Leu Ser			816
	260	265		270
40	ATT GTG CAT AGT TTG ATG TGC CAT AGA CAA GGT GGA GAG AGT GAA ACA Ile Val His Ser Leu Met Cys His Arg Gln Gly Glu Ser Glu Thr			864
	275	280		285
45	TTT GCA AAA AGA GCA ATT GAA AGT TTG GTA AAG AAG CTG AAG GAG AAA Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys Glu Lys			912
	290	295		300
50	AAA GAT GAA TTG GAT TCT TTA ATA ACA GCT ATA ACT ACA AAT GGA GCT Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn Gly Ala			960
	305	310	315	320
55	CAT CCT AGT AAA TGT GTT ACC ATA CAG AGA ACA TTG GAT GGG AGG CTT His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly Arg Leu			1008
	325	330		335
60	CAG GTG GCT GGT CGG AAA GGA TTT CCT CAT GTG ATC TAT GCC CGT CTC Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala Arg Leu			1056
	340	345		350
65	TGG AGG TGG CCT GAT CTT CAC AAA AAT GAA CTA AAA CAT GTT AAA TAT Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val Lys Tyr			1104
	355	360		365
70	TGT CAG TAT GCG TTT GAC TTA AAA TGT GAT AGT GTC TGT GTG AAT CCA Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val Asn Pro			1152
				105

		106		
	370	375	380	
5	TAT CAC TAC GAA CGA GTT GTA TCA CCT GGA ATT GAT CTC TCA GGA TTA Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser Gly Leu 385 390 395 400			1200
	ACA CTG CAG AGT AAT GCT CCA TCA AGT ATG ATG GTG AAG GAT GAA TAT Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp Glu Tyr 405 410 415			1248
10	GTG CAT GAC TTT GAG GGA CAG CCA TCG TTG TCC ACT GAA GGA CAT TCA Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly His Ser 420 425 430			1296
15	ATT CAA ACC ATC CAG CAT CCA CCA AGT AAT CGT GCA TCG ACA GAG ACA Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr Glu Thr 435 440 445			1344
20	TAC AGC ACC CCA GCT CTG TTA GCC CCA TCT GAG TCT AAT GCT ACC AGC Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala Thr Ser 450 455 460			1392
25	ACT GCC AAC TTT CCC AAC ATT CCT GTG GCT TCC ACA AGT CAG CCT GCC Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln Pro Ala 465 470 475 480			1440
	AGT ATA CTG GGG GGC AGC CAT AGT GAA GGA CTG TTG CAG ATA GCA TCA Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile Ala Ser 485 490 495			1488
30	GGG CCT CAG CCA GGA CAG CAG AAT GGA TTT ACT GGT CAG CCA GCT Gly Pro Gln Pro Gly Gln Gln Asn Gly Phe Thr Gly Gln Pro Ala 500 505 510			1536
35	ACT TAC CAT CAT AAC AGC ACT ACC ACC TGG ACT GGA AGT AGG ACT GCA Thr Tyr His His Asn Ser Thr Thr Trp Thr Gly Ser Arg Thr Ala 515 520 525			1584
40	CCA TAC ACA CCT AAT TTG CCT CAC CAC CAA AAC GGC CAT CTT CAG CAC Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu Gln His 530 535 540			1632
45	CAC CCG CCT ATG CCG CCC CAT CCC GGA CAT TAC TGG CCT GTT CAC AAT His Pro Pro Met Pro His Pro Gly His Tyr Trp Pro Val His Asn 545 550 555 560			1680
	GAG CTT GCA TTC CAG CCT CCC ATT TCC AAT CAT CCT GCT CCT GAG TAT Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro Glu Tyr 565 570 575			1728
50	TGG TGT TCC ATT GCT TAC TTT GAA ATG GAT GTT CAG GTA GGA GAG ACA Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly Glu Thr 580 585 590			1776
55	TTT AAG GTT CCT TCA AGC TGC CCT ATT GTT ACT GTT GAT GGA TAC GTG Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly Tyr Val			1824

107

	595	600	605	
5	GAC CCT TCT GGA GGA GAT CGC TTT TGT TTG GGT CAA CTC TCC AAT GTC Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser Asn Val 610 615 620			1872
10	CAC AGG ACA GAA GCC ATT GAG AGA GCA AGG TTG CAC ATA GGC AAA GGT His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly Lys Gly 625 630 635 640			1920
15	GTG CAG TTG GAA TGT AAA GGT GAA GGT GAT GTT TGG GTC AGG TGC CTT Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg Cys Leu 645 650 655			1968
20	AGT GAC CAC GCG GTC TTT GTA CAG AGT TAC TAC TTA GAC AGA GAA GCT Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg Glu Ala 660 665 670			2016
25	GGG CGT GCA CCT GGA GAT GCT GTT CAT AAG ATC TAC CCA AGT GCA TAT Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser Ala Tyr 675 680 685			2064
30	ATA AAG GTC TTT GAT TTG CGT CAG TGT CAT CGA CAG ATG CAG CAG CAG Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln Gln Gln 690 695 700			2112
35	GCG GCT ACT GCA CAA GCT GCA GCA GCT GCC CAG GCA GCA GCC GTG GCA Ala Ala Thr Ala Gln Ala Ala Ala Ala Gln Ala Ala Ala Val Ala 705 710 715 720			2160
40	GGA AAC ATC CCT GGC CCA GGA TCA GTA GGT GGA ATA GCT CCA GCT ATC Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro Ala Ile 725 730 735			2208
45	AGT CTG TCA GCT GCT GGA ATT GGT GTT GAT GAC CTT CGT CGC TTA Ser Leu Ser Ala Ala Gly Ile Gly Val Asp Asp Leu Arg Arg Leu 740 745 750			2256
50	TGC ATA CTC AGG ATG AGT TTT GTG AAA GGC TGG GGA CCG GAT TAC CCA Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp Tyr Pro 755 760 765			2304
55	AGA CAG AGC ATC AAA GAA ACA CCT TGC TGG ATT GAA ATT CAC TTA CAC Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His Leu His 770 775 780			2352
	CGG GCC CTC CAG CTC CTA GAC GAA GTA CTT CAT ACC ATG CCG ATT GCA Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro Ile Ala 785 790 795 800			2400
	GAC CCA CAA CCT TTA GAC TGA Asp Pro Gln Pro Leu Asp 805			2421

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10	15
15	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
	20	25	30
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
	35	40	45
20	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
	50	55	60
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
65	70	75	80
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
	85	90	95
25	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100	105	110
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
	115	120	125
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
30	130	135	140
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
145	150	155	160
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
	165	170	175
35	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
	180	185	190
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
	195	200	205
40	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
	210	215	220
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
225	230	235	240
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Asn Ser Thr Met Asp		
	245	250	255
45	Asn Met Ser Ile Thr Asn Thr Pro Thr Ser Asn Asp Ala Cys Leu Ser		
	260	265	270
	Ile Val His Ser Leu Met Cys His Arg Gln Gly Glu Ser Glu Thr		
	275	280	285
	Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys Glu Lys		
50	290	295	300
	Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn Gly Ala		
305	310	315	320
	His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly Arg Leu		
	325	330	335
55	Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala Arg Leu		
	340	345	350

109

Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val Lys Tyr
 355 360 365
 Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val Asn Pro
 370 375 380
 5 Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser Gly Leu
 385 390 395 400
 Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp Glu Tyr
 405 410 415
 10 Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly His Ser
 420 425 430
 Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr Glu Thr
 435 440 445
 Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala Thr Ser
 450 455 460
 15 Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln Pro Ala
 465 470 475 480
 Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile Ala Ser
 485 490 495
 20 Gly Pro Gln Pro Gly Gln Gln Gln Asn Gly Phe Thr Gly Gln Pro Ala
 500 505 510
 Thr Tyr His His Asn Ser Thr Thr Trp Thr Gly Ser Arg Thr Ala
 515 520 525
 Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu Gln His
 530 535 540
 25 His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val His Asn
 545 550 555 560
 Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro Glu Tyr
 565 570 575
 30 Trp Cys Ser Ile Tyr Phe Glu Met Asp Val Gln Val Gly Glu Thr
 580 585 590
 Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly Tyr Val
 595 600 605
 Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser Asn Val
 610 615 620
 35 His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly Lys Gly
 625 630 635 640
 Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg Cys Leu
 645 650 655
 Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg Glu Ala
 660 665 670
 40 Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser Ala Tyr
 675 680 685
 Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln Gln Gln
 690 695 700
 45 Ala Ala Thr Ala Gln Ala Ala Ala Ala Ala Gln Ala Ala Ala Val Ala
 705 710 715 720
 Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro Ala Ile
 725 730 735
 50 Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg Arg Leu
 740 745 750
 Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp Tyr Pro
 755 760 765
 Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His Leu His
 770 775 780
 55 Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro Ile Ala
 785 790 795 800

109

110

Asp Pro Gln Pro Leu Asp
805

(2) INFORMATION FOR SEQ ID NO:54:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

15

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...3117

(D) OTHER INFORMATION:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

110

111

	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
5	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720
30	GGA CTC AGA TCT ACC ATG GCG GGC TGG ATC CAG GCC CAG CAG CTG CAG Gly Leu Arg Ser Thr Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln 245 250 255	768
35	GGA GAC GCG CTG CGC CAG ATG CAG GTG CTG TAC GGC CAG CAC TTC CCC Gly Asp Ala Leu Arg Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro 260 265 270	816
40	ATC GAG GTC CGG CAC TAC TTG GCC CAG TGG ATT GAG AGC CAG CCA TGG Ile Glu Val Arg His Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp 275 280 285	864
45	GAT GCC ATT GAC TTG GAC AAT CCC CAG GAC AGA GGC CAA GCC ACC CAG Asp Ala Ile Asp Leu Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln 290 295 300	912
50	CTC CTG GAG GGC CTG GTG CAG GAG CTG CAG AAG AAG GCG GAG CAC CAG Leu Leu Glu Gly Leu Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln 305 310 315 320	960
55	GTG GGG GAA GAT GGG TTT TTA CTG AAG ATC AAG CTG GGG CAC TAC GCC Val Gly Glu Asp Gly Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala 325 330 335	1008
	ACG CAG CTC CAG AAA ACA TAT GAC CGC TGC CCC CTG GAG CTG GTC CGC Thr Gln Leu Gln Lys Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg 340 345 350	1056
	TGC ATC CGG CAC ATT CTG TAC AAT GAA CAG AGG CTG GTC CGA GAA GCC Cys Ile Arg His Ile Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala 355 360 365	1104

112

	AAC AAT TGC AGC TCT CCG GCT GGG ATC CTG GTT GAC GCC ATG TCC CAG Asn Asn Cys Ser Ser Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln 370 375 380	1152
5	AAG CAC CTT CAG ATC AAC CAG ACA TTT GAG GAG CTG CGA CTG GTC ACG Lys His Leu Gln Ile Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr 385 390 395 400	1200
10	CAG GAC ACA GAG AAT GAG CTG AAG AAA CTG CAG CAG ACT CAG GAG TAC Gln Asp Thr Glu Asn Glu Leu Lys Leu Gln Gln Thr Gln Glu Tyr 405 410 415	1248
15	TTC ATC ATC CAG TAC CAG GAG AGC CTG AGG ATC CAA GCT CAG TTT GCC Phe Ile Ile Gln Tyr Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala 420 425 430	1296
20	CAG CTG GCC CAG CTG AGC CCC CAG GAG CGT CTG AGC CGG GAG ACG GCC Gln Leu Ala Gln Leu Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala 435 440 445	1344
25	CTC CAG CAG AAG CAG GTG TCT CTG GAG GCC TGG TTG CAG CGT GAG GCA Leu Gln Gln Lys Gln Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala 450 455 460	1392
30	CAG ACA CTG CAG CAG TAC CGC GTG GAG CTG GCC GAG AAG CAC CAG AAG Gln Thr Leu Gln Gln Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys 465 470 475 480	1440
35	ACC CTG CAG CTG CTG CGG AAG CAG CAG ACC ATC ATC CTG GAT GAC GAG Thr Leu Gln Leu Leu Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu 485 490 495	1488
40	CTG ATC CAG TGG AAG CGG CGG CAG CAG CTG GCC GGG AAC GGC GGG CCC Leu Ile Gln Trp Lys Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro 500 505 510	1536
45	CCC GAG GGC AGC CTG GAC GTG CTA CAG TCC TGG TGT GAG AAG TTG GCC Pro Glu Gly Ser Leu Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala 515 520 525	1584
50	GAG ATC ATC TGG CAG AAC CGG CAG CAG ATC CGC AGG GCT GAG CAC CTC Glu Ile Ile Trp Gln Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu 530 535 540	1632
55	TGC CAG CAG CTG CCC ATC CCC GGC CCA GTG GAG GAG ATG CTG GCC GAG Cys Gln Gln Leu Pro Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu 545 550 555 560	1680
55	GTC AAC GCC ACC ATC ACG GAC ATT ATC TCA GCC CTG GTG ACC AGC ACA Val Asn Ala Thr Ile Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr 565 570 575	1728
55	TTC ATC ATT GAG AAG CAG CCT CCT CAG GTC CTG AAG ACC CAG ACC AAG Phe Ile Ile Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys 580 585 590	1776

112

113

	TTT GCA GCC ACC GTA CGC CTG CTG GTG GGC GGG AAG CTG AAC GTG CAC Phe Ala Ala Thr Val Arg Leu Leu Val Gly Gly Lys Leu Asn Val His 595 600 605	1824
5	ATG AAT CCC CCC CAG GTG AAG GCC ACC ATC ATC AGT GAG CAG CAG GCC Met Asn Pro Pro Gln Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala 610 615 620	1872
10	AAG TCT CTG CTT AAA AAT GAG AAC ACC CGC AAC GAG TGC AGT GGT GAG Lys Ser Leu Leu Lys Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu 625 630 635 640	1920
15	ATC CTG AAC AAC TGC TGC GTG ATG GAG TAC CAC CAA GCC ACG GGC ACC Ile Leu Asn Asn Cys Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr 645 650 655	1968
20	CTC AGT GCC CAC TTC AGG AAC ATG TCA CTG AAG AGG ATC AAG CGT GCT Leu Ser Ala His Phe Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala 660 665 670	2016
25	GAC CGG CGG GGT GCA GAG TCC GTG ACA GAG GAG AAG TTC ACA GTC CTG Asp Arg Arg Gly Ala Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu 675 680 685	2064
30	TTT GAG TCT CAG TTC AGT GTT GGC AGC AAT GAG CTT GTG TTC CAG GTG Phe Glu Ser Gln Phe Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val 690 695 700	2112
35	AAG ACT CTG TCC CTA CCT GTG GTT GTC ATC GTC CAC GGC AGC CAG GAC Lys Thr Leu Ser Leu Pro Val Val Val Ile Val His Gly Ser Gln Asp 705 710 715 720	2160
40	CAC AAT GCC ACG GCT ACT GTG CTG TGG GAC AAT GCC TTT GCT GAG CCG His Asn Ala Thr Ala Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro 725 730 735	2208
45	GGC AGG GTG CCA TTT GCC GTG CCT GAC AAA GTG CTG TGG CCG CAG CTG Gly Arg Val Pro Phe Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu 740 745 750	2256
50	TGT GAG GCG CTC AAC ATG AAA TTC AAG GCC GAA GTG CAG AGC AAC CGG Cys Glu Ala Leu Asn Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg 755 760 765	2304
55	GGC CTG ACC AAG GAG AAC CTC GTG TTC CTG GCG CAG AAA CTG TTC AAC Gly Leu Thr Lys Glu Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn 770 775 780	2352
	AAC AGC AGC AGC CAC CTG GAG GAC TAC AGT GGC CTG TCC GTG TCC TGG Asn Ser Ser Ser His Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp 785 790 795 800	2400
	TCC CAG TTC AAC AGG GAG AAC TTG CCG GGC TGG AAC TAC ACC TTC TGG Ser Gln Phe Asn Arg Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp 805 810 815	2448

114

	CAG TGG TTT GAC GGG GTG ATG GAG GTG TTG AAG AAG CAC CAC AAG CCC Gln Trp Phe Asp Gly Val Met Glu Val Leu Lys Lys His His Lys Pro 820 825 830	2496
5	CAC TGG AAT GAT GGG GCC ATC CTA GGT TTT GTG AAT AAG CAA CAG GCC His Trp Asn Asp Gly Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala 835 840 845	2544
10	CAC GAC CTG CTC ATC AAC AAG CCC GAC GGG ACC TTC TTG TTG CGC TTT His Asp Leu Leu Ile Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe 850 855 860	2592
15	AGT GAC TCA GAA ATC GGG GGC ATC ACC ATC GCC TGG AAG TTT GAC TCC Ser Asp Ser Glu Ile Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser 865 870 875 880	2640
20	CCG GAA CGC AAC CTG TGG AAC CTG AAA CCA TTC ACC ACG CGG GAT TTC Pro Glu Arg Asn Leu Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe 885 890 895	2688
25	TCC ATC AGG TCC CTG GCT GAC CGG CTG GGG GAC CTG AGC TAT CTC ATC Ser Ile Arg Ser Leu Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile 900 905 910	2736
30	TAT GTG TTT CCT GAC CGC CCC AAG GAT GAG GTC TTC TCC AAG TAC TAC Tyr Val Phe Pro Asp Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr 915 920 925	2784
35	ACT CCT GTG CTG GCT AAA GCT GTT GAT GGA TAT GTG AAA CCA CAG ATC Thr Pro Val Leu Ala Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile 930 935 940	2832
40	AAG CAA GTG GTC CCT GAG TTT GTG AAT GCA TCT GCA GAT GCT GGG GGC Lys Gln Val Val Pro Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly 945 950 955 960	2880
45	AGC AGC GCC ACG TAC ATG GAC CAG GCC CCC TCC CCA GCT GTG TGC CCC Ser Ser Ala Thr Tyr Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro 965 970 975	2928
50	CAG GCT CCC TAT AAC ATG TAC CCA CAG AAC CCT GAC CAT GTA CTC GAT Gln Ala Pro Tyr Asn Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp 980 985 990	2976
55	CAG GAT GGA GAA TTC GAC CTG GAT GAG ACC ATG GAT GTG GCC AGG CAC Gln Asp Gly Glu Phe Asp Leu Asp Glu Thr Met Asp Val Ala Arg His 995 1000 1005	3024
	GTG GAG GAA CTC TTA CGC CGA CCA ATG GAC AGT CTT GAC TCC CGC CTC Val Glu Glu Leu Leu Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu 1010 1015 1020	3072
	TCG CCC CCT GCC GGT CTT TTC ACC TCT GCC AGA GGC TCC CTC TCA TGA Ser Pro Pro Ala Gly Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser 1025 1030 1035	3120

1

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1039 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

15	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
	1	5	10
			15
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
	20	25	30
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
20	35	40	45
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
	50	55	60
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
	65	70	75
	80		
25	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
	85	90	95
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100	105	110
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
30	115	120	125
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
	130	135	140
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
	145	150	155
	160		
35	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
	165	170	175
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
	180	185	190
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
40	195	200	205
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
	210	215	220
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
	225	230	235
	240		
45	Gly Leu Arg Ser Thr Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln		
	245	250	255
	Gly Asp Ala Leu Arg Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro		
	260	265	270
	Ile Glu Val Arg His Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp		
50	275	280	285
	Asp Ala Ile Asp Leu Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln		
	290	295	300
	Leu Leu Glu Gly Leu Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln		
	305	310	315
	320		
55	Val Gly Glu Asp Gly Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala		
	325	330	335

Thr Gln Leu Gln Lys Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg
 340 345 350
 Cys Ile Arg His Ile Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala
 355 360 365
 5 Asn Asn Cys Ser Ser Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln
 370 375 380
 Lys His Leu Gln Ile Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr
 385 390 395 400
 10 Gln Asp Thr Glu Asn Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr
 405 410 415
 Phe Ile Ile Gln Tyr Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala
 420 425 430
 Gln Leu Ala Gln Leu Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala
 435 440 445
 15 Leu Gln Gln Lys Gln Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala
 450 455 460
 Gln Thr Leu Gln Gln Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys
 465 470 475 480
 Thr Leu Gln Leu Leu Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu
 20 485 490 495
 Leu Ile Gln Trp Lys Arg Arg Gln Gln Ile Arg Arg Ala Glu His Leu
 500 505 510
 Pro Glu Gly Ser Leu Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala
 515 520 525
 25 Glu Ile Ile Trp Gln Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu
 530 535 540
 Cys Gln Gln Leu Pro Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu
 545 550 555 560
 Val Asn Ala Thr Ile Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr
 30 565 570 575
 Phe Ile Ile Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys
 580 585 590
 Phe Ala Ala Thr Val Arg Leu Leu Val Gly Gly Lys Leu Asn Val His
 595 600 605
 35 Met Asn Pro Pro Gln Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala
 610 615 620
 Lys Ser Leu Leu Lys Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu
 625 630 635 640
 Ile Leu Asn Asn Cys Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr
 40 645 650 655
 Leu Ser Ala His Phe Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala
 660 665 670
 Asp Arg Arg Gly Ala Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu
 675 680 685
 45 Phe Glu Ser Gln Phe Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val
 690 695 700
 Lys Thr Leu Ser Leu Pro Val Val Val Ile Val His Gly Ser Gln Asp
 705 710 715 720
 His Asn Ala Thr Ala Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro
 50 725 730 735
 Gly Arg Val Pro Phe Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu
 740 745 750
 Cys Glu Ala Leu Asn Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg
 755 760 765
 55 Gly Leu Thr Lys Glu Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn
 770 775 780

117

	Asn Ser Ser Ser His Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp		
785	790	795	800
	Ser Gln Phe Asn Arg Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp		
	805	810	815
5	Gln Trp Phe Asp Gly Val Met Glu Val Leu Lys Lys His His Lys Pro		
	820	825	830
	His Trp Asn Asp Gly Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala		
	835	840	845
10	His Asp Leu Leu Ile Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe		
	850	855	860
	Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser		
865	870	875	880
	Pro Glu Arg Asn Leu Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe		
	885	890	895
15	Ser Ile Arg Ser Leu Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile		
	900	905	910
	Tyr Val Phe Pro Asp Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr		
	915	920	925
20	Thr Pro Val Leu Ala Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile		
	930	935	940
	Lys Gln Val Val Pro Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly		
945	950	955	960
	Ser Ser Ala Thr Tyr Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro		
	965	970	975
25	Gln Ala Pro Tyr Asn Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp		
	980	985	990
	Gln Asp Gly Glu Phe Asp Leu Asp Glu Thr Met Asp Val Ala Arg His		
	995	1000	1005
30	Val Glu Glu Leu Leu Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu		
	1010	1015	1020
	Ser Pro Pro Ala Gly Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser		
025	1030	1035	1

(2) INFORMATION FOR SEQ ID NO:56:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

45

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1872

(D) OTHER INFORMATION:

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATG	GCG	GCG	GCG	GCG	GCT	CCG	GGG	GGC	GGG	GAG	CCC	AGG	
Met	Ala	Ala	Ala	Ala	Ala	Pro	Gly	Gly	Gly	Gly	Glu	Pro	Arg
1						5						10	15

48

55

GGA	ACT	GCT	GGG	GTC	GTC	CCG	GTG	GTC	CCC	GGG	GAG	GTG	GAG	GTG	GTG
Gly	Thr	Ala	Gly	Val	Val	Pro	Val	Val	Pro	Gly	Glu	Val	Glu	Val	Val

96

117

	118			
	20	25	30	
5	AAG GGG CAG CCA TTC GAT GTG GGC CCA CGC TAC ACG CAG CTG CAG TAC Lys Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr 35 40 45			144
10	ATC GGC GAG GGC GCG TAC GGC ATG GTC AGC TCA GCT TAT GAC CAC GTG Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val 50 55 60			192
15	CGC AAG ACC AGA GTG GCC ATC AAG AAG ATC AGC CCC TTT GAG CAT CAA Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln 65 70 75 80			240
20	ACC TAC TGT CAG CGC ACG CTG AGG GAG ATC CAG ATC TTG CTG CGA TTC Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe 85 90 95			288
25	CGC CAT GAG AAT GTT ATA GGC ATC CGA GAC ATC CTC AGA GCG CCC ACC Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Pro Thr 100 105 110			336
30	CTG GAA GCC ATG AGA GAT GTT TAC ATT GTT CAG GAC CTC ATG GAG ACA Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr 115 120 125			384
35	GAC CTG TAC AAG CTG CTT AAA AGC CAG CAG CTG AGC AAT GAC CAC ATC Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile 130 135 140			432
40	TGC TAC TTC CTC TAC CAG ATC CTC CGG GGC CTC AAG TAT ATA CAC TCA Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser 145 150 155 160			480
45	GCC AAT GTG CTG CAC CGG GAC CTG AAG CCT TCC AAT CTG CTT ATC AAC Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn 165 170 175			528
50	ACC ACC TGC GAC CTT AAG ATC TGT GAT TTT GGC CTG GCC CGG ATT GCT Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala 180 185 190			576
55	GAC CCT GAG CAC GAC CAC ACT GGC TTT CTG ACG GAG TAT GTG GCC ACA Asp Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr 195 200 205			624
	CGC TGG TAC CGA GCC CCA GAG ATC ATG CTT AAT TCC AAG GGC TAC ACC Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr 210 215 220			672
	AAA TCC ATC GAC ATC TGG TCT GTG GGC TGC ATT CTG GCT GAG ATG CTC Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu 225 230 235 240			720
	TCC AAC CGG CCC ATC TTC CCC GGC AAG CAC TAC CTG GAC CAG CTC AAC Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn			768

	119		
	245	250	255
5	CAC ATT CTA GGT ATC TTG GGT TCC CCA TCC CAG GAG GAC CTT AAT TGC His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys 260 265 270		816
10	ATC ATT AAC ATG AAG GCC CGA AAC TAC CTG CAG TCT CTG CCC TCG AAA Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys 275 280 285		864
15	ACC AAG GTG GCT TGG GCC AAG CTC TTT CCT AAA TCT GAC TCC AAA GCT Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala 290 295 300		912
20	CTT GAC CTG CTG GAC CGG ATG TTA ACC TTC AAC CCA AAC AAG CGC ATC Leu Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile 305 310 315 320		960
25	ACA GTA GAG GAA GCG CTG GCT CAC CCT TAC CTG GAA CAG TAC TAC GAT Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp 325 330 335		1008
30	CCG ACA GAT GAG CCA GTG GCC GAG GAG CCA TTC ACC TTC GAC ATG GAG Pro Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Asp Met Glu 340 345 350		1056
35	CTG GAT GAC CTC CCC AAG GAG CGG CTG AAG GAG TTG ATC TTC CAG GAG Leu Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu 355 360 365		1104
40	ACA GCC CGC TTC CAG CCA GGG GCG CCA GAG GGC CCC GGG CGC GCC ATG Thr Ala Arg Phe Gln Pro Gly Ala Pro Glu Gly Pro Gly Arg Ala Met 370 375 380		1152
45	AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT CTT GTT GAA Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 385 390 395 400		1200
50	TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT AGT GGA GAG GGT Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu Gly 405 410 415		1248
55	GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT ATT TGC ACT Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 420 425 430		1296
	ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC ACT ACT CTC ACT Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr 435 440 445		1344
	TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT ATG AAA CAG CAT Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 450 455 460		1392
	GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG GAA AGA ACT Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr		1440

		120			
	465	470	475	480	
	ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT GAA GTC AAG Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys				1488
5	485	490	495		
	TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA GGT ATT GAT Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp				1536
	500	505	510		
10	TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG GAA TAC AAT TAT Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn Tyr				1584
	515	520	525		
15	AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA AAG AAT GGC ATC Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile				1632
	530	535	540		
20	AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT GGA AGC GTT CAA Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln				1680
	545	550	555	560	
25	TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT GGC CCT GTC Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val				1728
	565	570	575		
	TTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT GCC CTT TCC AAA Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys				1776
	580	585	590		
30	GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT GAG TTT GTA ACA Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr				1824
	595	600	605		
35	GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA CCT CAG GAG T Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Gln Glu				1873
	610	615	620		
	AA				1875
40	(2) INFORMATION FOR SEQ ID NO:57:				
	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 624 amino acids				
45	(B) TYPE: amino acid				
	(C) STRANDEDNESS: single				
	(D) TOPOLOGY: linear				
	(ii) MOLECULE TYPE: protein				
50	(v) FRAGMENT TYPE: internal				
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:				
	Met Ala Ala Ala Ala Ala Ala Pro Gly Gly Gly Gly Glu Pro Arg				
55	1	5	10	15	
	Gly Thr Ala Gly Val Val Pro Val Val Pro Gly Glu Val Glu Val Val				

121

	20	25	30
	Lys Gly Gln Pro Phe Asp Val	Gly Pro Arg Tyr Thr	Gln Leu Gln Tyr
	35	40	45
5	Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala	Tyr Asp His Val	
	50	55	60
	Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro	Phe Glu His Gln	
	65	70	75
	Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile	Leu Arg Phe	
	85	90	95
10	Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile	Leu Arg Ala Pro Thr	
	100	105	110
	Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp	Leu Met Glu Thr	
	115	120	125
15	Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu	Ser Asn Asp His Ile	
	130	135	140
	Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu	Lys Tyr Ile His Ser	
	145	150	155
	Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn	Leu Leu Ile Asn	
	165	170	175
20	Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly	Leu Ala Arg Ile Ala	
	180	185	190
	Asp Pro Glu His Asp His Thr Gly Phe Leu Thr	Glu Tyr Val Ala Thr	
	195	200	205
25	Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn	Ser Lys Gly Tyr Thr	
	210	215	220
	Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile	Leu Ala Glu Met Leu	
	225	230	235
	Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr	Leu Asp Gln Leu Asn	
	245	250	255
30	His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln	Glu Asp Leu Asn Cys	
	260	265	270
	Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln	Ser Leu Pro Ser Lys	
	275	280	285
35	Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys	Ser Asp Ser Lys Ala	
	290	295	300
	Leu Asp Leu Leu Asp Arg Met Leu Thr Phe Asn	Pro Asn Lys Arg Ile	
	305	310	315
	Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu	Glu Gln Tyr Tyr Asp	
	325	330	335
40	Pro Thr Asp Glu Pro Val Ala Glu Glu Pro Phe	Thr Phe Asp Met Glu	
	340	345	350
	Leu Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu	Leu Ile Phe Gln Glu	
	355	360	365
45	Thr Ala Arg Phe Gln Pro Gly Ala Pro Glu	Gly Pro Gly Arg Ala Met	
	370	375	380
	Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val	Pro Ile Leu Val Glu	
	385	390	395
	Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser	Val Ser Gly Glu Gly	
	405	410	415
50	Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu	Lys Phe Ile Cys Thr	
	420	425	430
	Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu	Val Thr Thr Leu Thr	
	435	440	445
55	Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp	His Met Lys Gln His	
	450	455	460
	Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	Tyr Val Gln Glu Arg Thr	

121

122

465	470	475	480
Ile Phe Tyr Lys Asp Asp Gly Asn Tyr	Lys Thr Arg Ala Glu Val Lys		
485	490	495	
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
500	505	510	
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn Tyr			
515	520	525	
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile			
530	535	540	
10 Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln			
545	550	555	560
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
565	570	575	
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
580	585	590	
Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr			
595	600	605	
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Gln Glu			
610	615	620	

20

(2) INFORMATION FOR SEQ ID NO:58:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1815 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: cDNA	
	(ix) FEATURE:	
	(A) NAME/KEY: Coding Sequence	
	(B) LOCATION: 1...1811	
	(D) OTHER INFORMATION:	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
40	ATG GCG GCG GCG GCG GCG GGC CCG GAG ATG GTC CGC GGG CAG GTG Met Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val 1 5 10 15	48
45	TTC GAC GTG GGG CCG CGC TAC ACT AAT CTC TCG TAC ATC GGA GAA GGC Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly 20 25 30	96
50	GCC TAC GGC ATG GTT TGT TCT GCT TAT GAT AAT CTC AAC AAA GTT CGA Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Leu Asn Lys Val Arg 35 40 45	144
55	GTT GCT ATC AAG AAA ATC AGT CCT TTT GAG CAC CAG ACC TAC TGT CAG Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln 50 55 60	192
	AGA ACC CTG AGA GAG ATA AAA ATC CTA CTG CGC TTC AGA CAT GAG AAC Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His Glu Asn 65 70 75 80	240

122

123

	ATC ATC GGC ATC AAT GAC ATC ATC CGG GCA CCA ACC ATT GAG CAG ATG Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu Gln Met 85 90 95	288
5	AAA GAT GTA TAT ATA GTA CAG GAC CTC ATG GAG ACA GAT CTT TAC AAG Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys 100 105 110	336
10	CTC TTG AAG ACA CAG CAC CTC AGC AAT GAT CAT ATC TGC TAT TTT CTT Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr Phe Leu 115 120 125	384
15	TAT CAG ATC CTG AGA GGA TTA AAG TAT ATA CAT TCA GCT AAT GTT CTG Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu 130 135 140	432
20	CAC CGT GAC CTC AAG CCT TCC AAC CTC CTG CTG AAC ACC ACT TGT GAT His Arg Asp Leu Lys Pro Ser Asn Leu Leu Asn Thr Thr Cys Asp 145 150 155 160	480
	CTC AAG ATC TGT GAC TTT GGC CTT GCC CGT GTT GCA GAT CCA GAC CAT Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro Asp His 165 170 175	528
25	GAT CAT ACA GGG TTC TTG ACA GAG TAT GTA GCC ACG CGT TGG TAC AGA Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg 180 185 190	576
30	GCT CCA GAA ATT ATG TTG AAT TCC AAG GGT TAT ACC AAG TCC ATT GAT Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp 195 200 205	624
35	ATT TGG TCT GTG GGC TGC ATC CTG GCA GAG ATG CTA TCC AAC AGG CCT Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro 210 215 220	672
40	ATC TTC CCA GGA AAG CAT TAC CTT GAC CAG CTG AAT CAC ATC CTG GGT Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly 225 230 235 240	720
	ATT CTT GGA TCT CCA TCA CAG GAA GAT CTG AAT TGT ATA ATA AAT TTA Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Leu 245 250 255	768
45	AAA GCT AGA AAC TAT TTG CTT TCT CTC CCG CAC AAA AAT AAG GTG CCG Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys Val Pro 260 265 270	816
50	TGG AAC AGG TTG TTC CCA AAC GCT GAC TCC AAA GCT CTG GAT TTA CTG Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp Leu Leu 275 280 285	864
55	GAT AAA ATG TTG ACA TTT AAC CCT CAC AAG AGG ATT GAA GTT GAA CAG Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val Glu Gln 290 295 300	912

123

124

	GCT CTG GCC CAC CCG TAC CTG GAG CAG TAT TAT GAC CCA AGT GAT GAG Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser Asp Glu 305 310 315 320	960
5	CCC ATT GCT GAA GCA CCA TTC AAG TTT GAC ATG GAG CTG GAC GAC TTA Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp Asp Leu 325 330 335	1008
10	CCT AAG GAG AAG CTC AAA GAA CTC ATT TTT GAA GAG ACT GCT CGA TTC Pro Lys Glu Lys Leu Glu Leu Ile Phe Glu Glu Thr Ala Arg Phe 340 345 350	1056
15	CAG CCA GGA TAC AGA TCT ATG GAT CCA CCG GTC GCC ACC ATG GTG AGC Gln Pro Gly Tyr Arg Ser Met Asp Pro Pro Val Ala Thr Met Val Ser 355 360 365	1104
20	AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu 370 375 380	1152
25	GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu 385 390 395 400	1200
30	GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC Gly Asp Ala Thr Tyr Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr 405 410 415	1248
35	GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr 420 425 430	1296
40	GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp 435 440 445	1344
45	TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile 450 455 460	1392
50	TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe 465 470 475 480	1440
55	GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe 485 490 495	1488
	AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn 500 505 510	1536
	AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys 515 520 525	1584

124

125

	GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC	1632
	Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu	
5	530 535 540	
	GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG	1680
	Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu	
	545 550 555 560	
10	CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC	1728
	Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp	
	565 570 575	
15	CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC	1776
	Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala	
	580 585 590	
20	GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AA GTAA	1815
	Ala Gly Ile Thr Leu .Gly Met Asp Glu Leu Tyr Lys	
	595 600	

(2) INFORMATION FOR SEQ ID NO:59:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 604 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: protein	
	(v) FRAGMENT TYPE: internal	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
	Met Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val	
	1 5 10 15	
	Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly	
	20 25 30	
40	Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Leu Asn Lys Val Arg	
	35 40 45	
	Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln	
	50 55 60	
	Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His Glu Asn	
45	65 70 75 80	
	Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu Gln Met	
	85 90 95	
	Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys	
	100 105 110	
50	Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr Phe Leu	
	115 120 125	
	Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu	
	130 135 140	
55	His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Thr Thr Cys Asp	
	145 150 155 160	
	Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro Asp His	

125

126

	165	170	175
	Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg		
	180	185	190
5	Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp		
	195	200	205
	Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro		
	210	215	220
	Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly		
	225	230	235
10	Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Leu		
	245	250	255
	Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys Val Pro		
	260	265	270
15	Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp Leu Leu		
	275	280	285
	Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val Glu Gln		
	290	295	300
	Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser Asp Glu		
	305	310	315
20	Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp Asp Leu		
	325	330	335
	Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala Arg Phe		
	340	345	350
	Gln Pro Gly Tyr Arg Ser Met Asp Pro Pro Val Ala Thr Met Val Ser		
	355	360	365
25	Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu		
	370	375	380
	Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu		
	385	390	395
30	Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr		
	405	410	415
	Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Leu Thr Tyr		
	420	425	430
35	Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp		
	435	440	445
	Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile		
	450	455	460
	Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe		
	465	470	475
40	Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe		
	485	490	495
	Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn		
	500	505	510
45	Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys		
	515	520	525
	Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu		
	530	535	540
	Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu		
	545	550	555
50	Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp		
	565	570	575
	Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala		
	580	585	590
55	Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	595	600	

127

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2508

(D) OTHER INFORMATION:

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATG GAG CTG GAA AAC ATC GTG GCC AAC ACG GTC TTG CTG AAA GCC AGG	48
Met Glu Leu Glu Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg	
20 1 5 10 15	

GAA GGG GGC GGA GGA AAG CGC AAA GGG AAA AGC AAG AAG TGG AAA GAA	96
Glu Gly Gly Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu	
20 25 30	

ATC CTG AAG TTC CCT CAC ATT AGC CAG TGT GAA GAC CTC CGA AGG ACC	144
Ile Leu Lys Phe Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr	
35 40 45	

ATA GAC AGA GAT TAC TGC AGT TTA TGT GAC AAG CAG CCA ATC GGG AGG	192
Ile Asp Arg Asp Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg	
50 55 60	

CTG CTT TTC CGG CAG TTT TGT GAA ACC AGG CCT GGG CTG GAG TGT TAC	240
Leu Leu Phe Arg Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr	
65 70 75 80	

ATT CAG TTC CTG GAC TCC GTG GCA GAA TAT GAA GTT ACT CCA GAT GAA	288
Ile Gln Phe Leu Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu	
85 90 95	

AAA CTG GGA GAG AAA GGG AAG GAA ATT ATG ACC AAG TAC CTC ACC CCA	336
Lys Leu Gly Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro	
100 105 110	

AAG TCC CCT GTT TTC ATA GCC CAA GTT GGC CAA GAC CTG GTC TCC CAG	384
Lys Ser Pro Val Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln	
115 120 125	

ACG GAG GAG AAG CTC CTA CAG AAG CCG TGC AAA GAA CTC TTT TCT GCC	432
Thr Glu Glu Lys Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala	
130 135 140	

TGT GCA CAG TCT GTC CAC GAG TAC CTG AGG GGA GAA CCA TTC CAC GAA	480
Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu	
145 150 155 160	

127

128

	TAT CTG GAC AGC ATG TTT TTT GAC CGC TTT CTC CAG TGG AAG TGG TTG Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu 165 170 175	528
5	GAA AGG CAA CCG GTG ACC AAA AAC ACT TTC AGG CAG TAT CGA GTG CTA Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu 180 185 190	576
10	GGA AAA GGG GGC TTC GGG GAG GTC TGT GCC TGC CAG GTT CGG GCC ACG Gly Lys Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr 195 200 205	624
15	GGT AAA ATG TAT GCC TGC AAG CGC TTG GAG AAG AAG AGG ATC AAA AAG Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys 210 215 220	672
20	AGG AAA GGG GAG TCC ATG GCC CTC AAT GAG AAG CAG ATC CTC GAG AAG Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys 225 230 235 240	720
	GTC AAC AGT CAG TTT GTG GTC AAC CTG GCC TAT GCC TAC GAG ACC AAG Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys 245 250 255	768
25	GAT GCA CTG TGC TTG GTC CTG ACC ATC ATG AAT GGG GGT GAC CTG AAG Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys 260 265 270	816
30	TTC CAC ATC TAC AAC ATG GGC AAC CCT GGC TTC GAG GAG GAG CGG GCC Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala 275 280 285	864
35	TTG TTT TAT GCG GCA GAG ATC CTC TGC GGC TTA GAA GAC CTC CAC CGT Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg 290 295 300	912
40	GAG AAC ACC GTC TAC CGA GAT CTG AAA CCT GAA AAC ATC CTG TTA GAT Glu Asn Thr Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp 305 310 315 320	960
	GAT TAT GGC CAC ATT AGG ATC TCA GAC CTG GGC TTG GCT GTG AAG ATC Asp Tyr Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile 325 330 335	1008
45	CCC GAG GGA GAC CTG ATC CGC GGC CGG GTG GGC ACT GTT GGC TAC ATG Pro Glu Gly Asp Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met 340 345 350	1056
50	GCC CCC GAA GTC CTG AAC AAC CAG AGG TAC GGC CTG AGC CCC GAC TAC Ala Pro Glu Val Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr 355 360 365	1104
55	TGG GGC CTT GGC TGC CTC ATC TAT GAG ATG ATC GAG GGC CAG TCG CCG Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro 370 375 380	1152

128

	TTC CGC GGC CGT AAG GAG AAG GTG AAG CGG GAG GTG GAC CGC CGG Phe Arg Gly Arg Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg 385	390	395	400	1200
5	GTC CTG GAG ACG GAG GAG GTG TAC TCC CAC AAG TTC TCC GAG GAG GCC Val Leu Glu Thr Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala 405	410		415	1248
10	AAG TCC ATC TGC AAG ATG CTG CTC ACG AAA GAT GCG AAG CAG AGG CTG Lys Ser Ile Cys Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu 420	425	430		1296
15	GGC TGC CAG GAG GAG GGG GCT GCA GAG GTC AAG AGA CAC CCC TTC TTC Gly Cys Gln Glu Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe 435	440	445		1344
20	AGG AAC ATG AAC TTC AAG CGC TTA GAA GCC GGG ATG TTG GAC CCT CCC Arg Asn Met Asn Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro 450	455	460		1392
25	TTC GTT CCA GAC CCC CGC GCT GTG TAC TGT AAG GAC GTG CTG GAC ATC Phe Val Pro Asp Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile 465	470	475	480	1440
30	GAG CAG TTC TCC ACT GTG AAG GGC GTC AAT CTG GAC CAC ACA GAC GAC Glu Gln Phe Ser Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp 485	490	495		1488
35	GAC TTC TAC TCC AAG TTC TCC ACG GGC TCT GTG TCC ATC CCA TGG CAA Asp Phe Tyr Ser Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln 500	505	510		1536
40	AAC GAG ATG ATA GAA ACA GAA TGC TTT AAG GAG CTG AAC GTG TTT GGA Asn Glu Met Ile Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly 515	520	525		1584
45	CCT AAT GGT ACC CTC CCG CCA GAT CTG AAC AGA AAC CAC CCT CCG GAA Pro Asn Gly Thr Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu 530	535	540		1632
50	CCG CCC AAG AAA GGG CTG CTC CAG AGA CTC TTC AAG CGG CAG CAT CAG Pro Pro Lys Lys Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln 545	550	555	560	1680
55	AAC AAT TCC AAG AGT TCG CCC AGC TCC AAG ACC AGT TTT AAC CAC CAC Asn Asn Ser Lys Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His 565	570	575		1728
580	ATA AAC TCA AAC CAT GTC AGC TCG AAC TCC ACC GGA AGC AGC AGG GAT Ile Asn Ser Asn His Val Ser Ser Asn Ser Thr Gly Ser Ser Arg Asp 585	590			1776
595	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly 600	605			1824

130

	GTC GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys 610 615 620	1872
5	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG Phe Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu 625 630 635 640	1920
10	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro 645 650 655	1968
15	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr 660 665 670	2016
20	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu 675 680 685	2064
	GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr 690 695 700	2112
25	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg 705 710 715 720	2160
30	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly 725 730 735	2208
35	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala 740 745 750	2256
40	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn 755 760 765	2304
	ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr 770 775 780	2352
45	CCC ATC GGC GAC GGC CCC GTG CTG CCC GAC AAC CAC TAC CTG AGC Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser 785 790 795 800	2400
50	ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met 805 810 815	2448
55	GTC CTG CTG GAG TTC GTG ACC GCC GGG ATC ACT CTC GGC ATG GAC Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp 820 825 830	2496

130

GAG CTG TAC AAG TAA
 Glu Leu Tyr Lys
 835

2511

5

(2) INFORMATION FOR SEQ ID NO:61:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 836 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

20 Met Glu Leu Glu Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg
 1 5 10 15
 Glu Gly Gly Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu
 20 25 30
 Ile Leu Lys Phe Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr
 35 40 45
 Ile Asp Arg Asp Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
 50 55 60
 Leu Leu Phe Arg Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr
 65 70 75 80
 Ile Gln Phe Leu Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu
 85 90 95
 Lys Leu Gly Glu Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro
 100 105 110
 Lys Ser Pro Val Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln
 115 120 125
 Thr Glu Glu Lys Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala
 130 135 140
 Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu
 145 150 155 160
 Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu
 165 170 175
 Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu
 180 185 190
 Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr
 195 200 205
 Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys
 210 215 220
 Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys
 225 230 235 240
 Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys
 245 250 255
 Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys
 260 265 270
 Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala
 275 280 285
 Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg

132

	290	295	300
	Glu Asn Thr Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp		
5	305	310	315
	Asp Tyr Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile		320
	325	330	335
	Pro Glu Gly Asp Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met		
	340	345	350
10	Ala Pro Glu Val Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr		
	355	360	365
	Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro		
	370	375	380
	Phe Arg Gly Arg Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg		
	385	390	395
	Val Leu Glu Thr Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala		400
15	405	410	415
	Lys Ser Ile Cys Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu		
	420	425	430
	Gly Cys Gln Glu Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe		
	435	440	445
20	Arg Asn Met Asn Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro		
	450	455	460
	Phe Val Pro Asp Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile		
	465	470	475
	Glu Gln Phe Ser Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp		480
25	485	490	495
	Asp Phe Tyr Ser Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln		
	500	505	510
	Asn Glu Met Ile Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly		
	515	520	525
30	Pro Asn Gly Thr Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu		
	530	535	540
	Pro Pro Lys Lys Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln		
	545	550	555
	Asn Asn Ser Lys Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His		560
35	565	570	575
	Ile Asn Ser Asn His Val Ser Ser Asn Ser Thr Gly Ser Ser Arg Asp		
	580	585	590
	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly		
	595	600	605
40	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys		
	610	615	620
	Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu		
	625	630	635
	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro		640
45	645	650	655
	Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr		
	660	665	670
	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu		
	675	680	685
50	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr		
	690	695	700
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg		
	705	710	715
	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly		720
55	725	730	735
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala		

133

	740	745	750
	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn		
	755	760	765
5	Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr		
	770	775	780
	Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser		
	785	790	795
	Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met		
	805	810	815
10	Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp		
	820	825	830
	Glu Leu Tyr Lys		
	835		

15 (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1893 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1890
 - (D) OTHER INFORMATION:

25 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATG AGC AGA AGC AAG CGT GAC AAC AAT TTT TAT AGT GTA GAG ATT GGA	48
Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly	
1 5 10 15	
35 GAT TCT ACA TTC ACA GTC CTG AAA CGA TAT CAG AAT TTA AAA CCT ATA	96
Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile	
20 25 30	
40 GGC TCA GGA GCT CAA GGA ATA GTA TGC GCA GCT TAT GAT GCC ATT CTT	144
Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu	
35 40 45	
45 GAA AGA AAT GTT GCA ATC AAG AAG CTA AGC CGA CCA TTT CAG AAT CAG	192
Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln	
50 55 60	
50 ACT CAT GCC AAG CGG GCC TAC AGA GAG CTA GTT CTT ATG AAA TGT GTT	240
Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val	
65 70 75 80	
55 AAT CAC AAA AAT ATA ATT GGC CTT TTG AAT GTT TTC ACA CCA CAG AAA	288
Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys	
85 90 95	
55 TCC CTA GAA GAA TTT CAA GAT GTT TAC ATA GTC ATG GAG CTC ATG GAT	336

133

134

	Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp		
	100	105	110
5	GCA AAT CTT TGC CAA GTG ATT CAG ATG GAG CTA GAT CAT GAA AGA ATG Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met		384
	115	120	125
10	TCC TAC CTT CTC TAT CAG ATG CTG TGT GGA ATC AAG CAC CTT CAT TCT Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser		432
	130	135	140
15	GCT GGA ATT ATT CAT CGG GAC TTA AAG CCC AGT AAT ATA GTA GTA AAA Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys		480
	145	150	155
	160		
20	TCT GAT TGC ACT TTG AAG ATT CTT GAC TTC GGT CTG GCC AGG ACT GCA Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala		528
	165	170	175
25	GGA ACG AGT TTT ATG ATG ACG CCT TAT GTA GTG ACT CGC TAC TAC AGA Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg		576
	180	185	190
30	GCA CCC GAG GTC ATC CTT GGC ATG GGC TAC AAG GAA AAC GTG GAT TTA Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Leu		624
	195	200	205
35	TGG TCT GTG GGG TGC ATT ATG GGA GAA ATG GTT TGC CAC AAA ATC CTC Trp Ser Val Gly Cys Ile Met Gly Glu Met Val Cys His Lys Ile Leu		672
	210	215	220
40	TTT CCA GGA AGG GAC TAT ATT GAT CAG TGG AAT AAA GTT ATT GAA CAG Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu Gln		720
	225	230	235
	240		
45	TCT GGA ACA CCA TGT CCT GAA TTC ATG AAG AAA CTG CAA CCA ACA GTA Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val		768
	245	250	255
50	AGG ACT TAC GTT GAA AAC AGA CCT AAA TAT GCT GGA TAT AGC TTT GAG Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu		816
	260	265	270
55	AAA CTC TTC CCT GAT GTC CTT TTC CCA GCT GAC TCA GAA CAC AAC AAA Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys		864
	275	280	285
	290	295	300
	305	310	315
	320		
	GAT GCA TCT AAA AGG ATC TCT GTA GAT GAA GCT CTC CAA CAC CCG TAC Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr		960
	305	310	315
	320		
	ATC AAT GTC TGG TAT GAT CCT TCT GAA GCA GAA GCT CCA CCA CCA AAG		1008

134

	135			
	Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys			
	325	330	335	
5	ATC CCT GAC AAG CAG TTA GAT GAA AGG GAA CAC ACA ATA GAA GAG TGG Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp	1056		
	340	345	350	
10	AAA GAA TTG ATA TAT AAG GAA GTT ATG GAC TTG GAG GAG AGA ACC AAG Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Arg Thr Lys	1104		
	355	360	365	
15	AAT GGA GTT ATA CGG GGG CAG CCC TCT CCT TTA GCA CAG GTG CAG CAG Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Ala Gln Val Gln Gln	1152		
	370	375	380	
20	TGG GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC Trp Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe	1200		
	385	390	395	400
25	ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly	1248		
	405	410	415	
30	CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly	1296		
	420	425	430	
35	AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro	1344		
	435	440	445	
40	TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC Trp Pro Thr Leu Val Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser	1392		
	450	455	460	
45	CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met	1440		
	465	470	475	480
50	CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly	1488		
	485	490		
55	AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val	1536		
	500	505	510	
50	AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile	1584		
	515	520	525	
55	CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile	1632		
	530	535	540	
	ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC	1680		

136

	Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg			
	545	550	555	560
5	CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG			1728
	His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln			
	565	570	575	
10	AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC			1776
	Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr			
	580	585	590	
15	CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT			1824
	Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp			
	595	600	605	
20	CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC			1872
	His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly			
	610	615	620	
25	ATG GAC GAG CTG TAC AAG TAA			1893
	Met Asp Glu Leu Tyr Lys			
	625	630		

25 (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

	Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly			
	1	5	10	15
40	Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile			
	20	25	30	
	Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu			
	35	40	45	
45	Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln			
	50	55	60	
	Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val			
	65	70	75	80
	Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys			
	85	90	95	
50	Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp			
	100	105	110	
	Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met			
	115	120	125	
55	Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser			
	130	135	140	
	Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys			

137

	145	150	155	160
	Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala			
	165	170	175	
5	Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg			
	180	185	190	
	Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Leu			
	195	200	205	
	Trp Ser Val Gly Cys Ile Met Gly Glu Met Val Cys His Lys Ile Leu			
	210	215	220	
10	Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu Gln			
	225	230	235	240
	Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val			
	245	250	255	
	Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu			
15	260	265	270	
	Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys			
	275	280	285	
	Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile			
	290	295	300	
20	Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr			
	305	310	315	320
	Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys			
	325	330	335	
	Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp			
25	340	345	350	
	Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys			
	355	360	365	
	Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Ala Gln Val Gln Gln			
	370	375	380	
30	Trp Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe			
	385	390	395	400
	Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly			
	405	410	415	
	His Lys Phe Ser Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly			
35	420	425	430	
	Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro			
	435	440	445	
	Trp Pro Thr Leu Val Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser			
	450	455	460	
40	Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met			
	465	470	475	480
	Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly			
	485	490	495	
	Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val			
45	500	505	510	
	Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile			
	515	520	525	
	Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile			
	530	535	540	
50	Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg			
	545	550	555	560
	His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln			
	565	570	575	
	Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr			
55	580	585	590	
	Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp			

138

595	600	605
His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly		
610	615	620
Met Asp Glu Leu Tyr Lys		
5	625	630

(2) INFORMATION FOR SEQ ID NO:64:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1821 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1818
 (D) OTHER INFORMATION:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

	ATG TCT CAG GAG AGG CCC ACG TTC TAC CGG CAG CTG AAC AAG ACA	48
25	Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr	
	1 5 10 15	
	ATC TGG GAG GTG CCC GAG CGT TAC CAG AAC CTG TCT CCA GTG GGC TCT	96
	Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser	
30	20 25 30	
	GGC GCC TAT GGC TCT GTG TGT GCT GCT TTT GAC ACA AAA ACG GGG TTA	144
	Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly Leu	
	35 40 45	
35	CGT GTG GCA GTG AAG AAG CTC TCC AGA CCA TTT CAG TCC ATC ATT CAT	192
	Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His	
	50 55 60	
40	GCG AAA AGA ACC TAC AGA GAA CTG CGG TTA CTT AAA CAT ATG AAA CAT	240
	Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His	
	65 70 75 80	
45	GAA AAT GTG ATT GGT CTG TTG GAC GTT TTT ACA CCT GCA AGG TCT CTG	288
	Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu	
	85 90 95	
50	GAG GAA TTC AAT GAT GTG TAT CTG GTG ACC CAT CTC ATG GGG GCA GAT	336
	Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp	
	100 105 110	
55	CTG AAC AAC ATT GTG AAA TGT CAG AAG CTT ACA GAT GAC CAT GTT CAG	384
	Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln	
	115 120 125	
	TTC CTT ATC TAC CAA ATT CTC CGA GGT CTA AAG TAT ATA CAT TCA GCT	432

139

	Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala		
	130	135	140
5	GAC ATA ATT CAC AGG GAC CTA AAA CCT AGT AAT CTA GCT GTG AAT GAA Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu		480
	145	150	155
10	160		
	GAC TGT GAG CTG AAG ATT CTG GAT TTT GGA CTG GCT CGG CAC ACA GAT Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp		528
	165	170	175
	GAT GAA ATG ACA GGC TAC GTG GCC ACT AGG TGG TAC AGG GCT CCT GAG Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu		576
15	180	185	190
	ATC ATG CTG AAC TGG ATG CAT TAC AAC CAG ACA GTT GAT ATT TGG TCA Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser		624
	195	200	205
20	GTG GGA TGC ATA ATG GCC GAG CTG TTG ACT GGA AGA ACA TTG TTT CCT Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro		672
	210	215	220
25	225	230	235
	240		
	GGT ACA GAC CAT ATT GAT CAG TTG AAG CTC ATT TTA AGA CTC GTT GGA Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly		720
	245	250	255
30	ACC CCA GGG GCT GAG CTT TTG AAG AAA ATC TCC TCA GAG TCT GCA AGA Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg		768
	260	265	270
35	275	280	285
	GTA TTT ATT GGT GCC AAT CCC CTG GCT GTC GAC TTG CTG GAG AAG ATG Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met		864
	290	295	300
40	CAT GCC TAC TTT GCT CAG TAC CAC GAT CCT GAT GAT GAA CCA GTG GCC His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala		912
	305	310	315
	320		
	CAT GCG TAT GAT CAG TCC TTT GAA AGC AGG GAC CTC CTT ATA GAT GAG Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu		960
45	325	330	335
	340	345	350
50	GAT CCT TAT GAT CAG TCC TTT GAA AGC AGG GAC CTC CTT ATA GAT GAG Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu		1008
	340	345	350
	TGG AAA AGC CTG ACC TAT GAT GAA GTC ATC AGC TTT GTG CCA CCA CCC Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro		1056
55	340	345	350
	CTT GAC CAA GAA GAG ATG GAG TCC GAG GAT CCA CCG GTC GCC ACC ATG		1104

139

140

	Leu Asp Gln Glu Glu Met Glu Ser Glu Asp Pro Pro Val Ala Thr Met		
	355	360	365
5	GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		1152
	370	375	380
10	GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		1200
	385	390	395
	400		
15	GCG GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		1248
	405	410	415
20	ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		1296
	420	425	430
25	435	440	445
30	ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		1344
	450	455	460
35	CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		1392
	485	490	495
40	ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		1440
	465	470	475
	480		
45	AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		1488
	500	505	510
50	GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		1536
	515	520	525
55	TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		1584
	530	535	540
	545	550	555
	560		
	CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		1680
	565	570	575
	580		
	GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		1728
	595	600	605
	610		
	AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG		1776

140

141

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
580	585	590
ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA		
5 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		1821
595	600	605

10 (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr			
1	5	10	15
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser			
25 20	25	30	
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly Leu			
35 35	40	45	
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His			
50 50	55	60	
30 Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His			
65 65	70	75	80
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu			
85 85	90	95	
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp			
35 100	105	110	
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln			
115 115	120	125	
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala			
130 130	135	140	
40 Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu			
145 145	150	155	160
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp			
165 165	170	175	
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu			
45 180	185	190	
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser			
195 195	200	205	
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro			
210 210	215	220	
50 Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly			
225 225	230	235	240
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg			
245 245	250	255	
Asn Tyr Ile Gln Ser Leu Thr Gln Met Pro Lys Met Asn Phe Ala Asn			
55 260	265	270	
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met			

142

	275	280	285
	Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala		
	290	295	300
5	His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala		
	305	310	315
	Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu		
	325	330	335
	Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro		
	340	345	350
10	Leu Asp Gln Glu Glu Met Glu Ser Glu Asp Pro Pro Val Ala Thr Met		
	355	360	365
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
	370	375	380
15	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
	385	390	395
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
	405	410	415
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
	420	425	430
20	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		
	435	440	445
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
	450	455	460
25	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
	465	470	475
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
	485	490	495
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
	500	505	510
30	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
	515	520	525
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
	530	535	540
35	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
	545	550	555
	Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
	565	570	575
	Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
	580	585	590
40	Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	595	600	605

(2) INFORMATION FOR SEQ ID NO:66:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2913 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

55 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2910
 (D) OTHER INFORMATION:

143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

5	ATG AGT GCT GAG GGG TAC CAG TAC AGA GCG CTG TAT GAT TAT AAA AAG Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys 1 5 10 15	48
10	GAA AGA GAA GAA GAT ATT GAC TTG CAC TTG GGT GAC ATA TTG ACT GTG Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val 20 25 30	96
15	AAT AAA GGG TCC TTA GTA GCT CTT GGA TTC AGT GAT GGA CAG GAA GCC Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala 35 40 45	144
20	AGG CCT GAA GAA ATT GGC TGG TTA AAT GGC TAT AAT GAA ACC ACA GGG Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly 50 55 60	192
25	GAA AGG GGG GAC TTT CCG GGA ACT TAC GTA GAA TAT ATT GGA AGG AAA Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys 65 70 75 80	240
30	AAA ATC TCG CCT CCC ACA CCA AAG CCC CGG CCA CCT CGG CCT CTT CCT Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro 85 90 95	288
35	GTT GCA CCA GGT TCT TCG AAA ACT GAA GCA GAT GTT GAA CAA CAA GCT Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala 100 105 110	336
40	TTG ACT CTC CCG GAT CTT GCA GAG CAG TTT GCC CCT CCT GAC ATT GCC Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala 115 120 125	384
45	CCG CCT CTT CTT ATC AAG CTC GTG GAA GCC ATT GAA AAG AAA GGT CTG Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Gly Leu 130 135 140	432
50	GAA TGT TCA ACT CTA TAC AGA ACA CAG AGC TCC AGC AAC CTG GCA GAA Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Asn Leu Ala Glu 145 150 155 160	480
55	TTA CGA CAG CTT CTT GAT TGT GAT ACA CCC TCC GTG GAC TTG GAA ATG Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met 165 170 175	528
60	ATC GAT GTG CAC GTT TTG GCT GAC GCT TTC AAA CGC TAT CTC CTG GAC Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp 180 185 190	576
65	TTA CCA AAT CCT GTC ATT CCA GCA GCC GTT TAC AGT GAA ATG ATT TCT Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser 195 200 205	624
70	TTA GCT CCA GAA GTA CAA AGC TCC GAA GAA TAT ATT CAG CTA TTG AAG	672

144

	Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile Gln Leu Leu Lys		
	210	215	220
5	AAG CTT ATT AGG TCG CCT AGC ATA CCT CAT CAG TAT TGG CTT ACG CTT Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr Trp Leu Thr Leu		720
	225	230	235
10	CAG TAT TTG TTA AAA CAT TTC TTC AAG CTC TCT CAA ACC TCC AGC AAA Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln Thr Ser Ser Lys		768
	245	250	255
15	AAT CTG TTG AAT GCA AGA GTA CTC TCT GAA ATT TTC AGC CCT ATG CTT Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe Ser Pro Met Leu		816
	260	265	270
20	TTC AGA TTC TCA GCA GCC AGC TCT GAT AAT ACT GAA AAC CTC ATA AAA Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu Asn Leu Ile Lys		864
	275	280	285
25	GTT ATA GAA ATT TTA ATC TCA ACT GAA TGG AAT GAA CGA CAG CCT GCA Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu Arg Gln Pro Ala		912
	290	295	300
30	CCA GCA CTG CCT CCT AAA CCA CCA AAA CCT ACT ACT GTA GCC AAC AAC Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn		960
	305	310	315
	320		
35	GGT ATG AAT AAC AAT ATG TCC TTA CAA AAT GCT GAA TGG TAC TGG GGA Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu Trp Tyr Trp Gly		1008
	325	330	335
40	GAT ATC TCG AGG GAA GAA GTG AAT GAA AAA CTT CGA GAT ACA GCA GAC Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp		1056
	340	345	350
45	GGG ACC TTT TTG GTA CGA GAT GCG TCT ACT AAA ATG CAT GGT GAT TAT Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr		1104
	355	360	365
50	ACT CTT ACA CTA AGG AAA GGG GGA AAT AAC AAA TTA ATC AAA ATA TTT Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe		1152
	370	375	380
55	CAT CGA GAT GGG AAA TAT GGC TTC TCT GAC CCA TTA ACC TTC AGT TCT His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser		1200
	385	390	395
	400		
60	GTG GTT GAA TTA ATA AAC CAC TAC CGG AAT GAA TCT CTA GCT CAG TAT Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr		1248
	405	410	415
65	AAT CCC AAA TTG GAT GTG AAA TTA CTT TAT CCA GTA TCC AAA TAC CAA Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln		1296
	420	425	430
70	CAG GAT CAA GTT GTC AAA GAA GAT AAT ATT GAA GCT GTA GGG AAA AAA		1344

145

	Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys		
	435	440	445
5	TTA CAT GAA TAT AAC ACT CAG TTT CAA GAA AAA AGT CGA GAA TAT GAT Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp		1392
	450	455	460
10	AGA TTA TAT GAA GAA TAT ACC CGC ACA TCC CAG GAA ATC CAA ATG AAA Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys		1440
	465	470	475
	480		
15	AGG ACA GCT ATT GAA GCA TTT AAT GAA ACC ATA AAA ATA TTT GAA GAA Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu		1488
	485	490	495
20	CAG TGC CAG ACC CAA GAG CGG TAC AGC AAA GAA TAC ATA GAA AAG TTT Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe		1536
	500	505	510
25	AAA CGT GAA GGC AAT GAG AAA GAA ATA CAA AGG ATT ATG CAT AAT TAT Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr		1584
	515	520	525
30	GAT AAG TTG AAG TCT CGA ATC AGT GAA ATT ATT GAC AGT AGA AGA AGA Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg		1632
	530	535	540
35	TTG GAA GAA GAC TTG AAG AAG CAG GCA GCT GAG TAT CGA GAA ATT GAC Leu Glu Glu Asp Leu Lys Glu Gln Ala Ala Glu Tyr Arg Glu Ile Asp		1680
	545	550	555
	560		
40	AAA CGT ATG AAC AGC ATT AAA CCA GAC CTT ATC CAG CTG AGA AAG ACG Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr		1728
	565	570	575
45	580	585	590
50	AGA GAC CAA TAC TTG ATG TGG TTG ACT CAA AAA GGT GTT CGG CAA AAG Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys		1776
	595	600	605
55	AAG TTG AAC GAG TGG TTG GGC AAT GAA AAC ACT GAA GAC CAA TAT TCA Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser		1824
	610	615	620
55	CTG GTG GAA GAT GAT GAA GAT TTG CCC CAT CAT GAT GAG AAG ACA TGG Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp		1872
	625	630	635
	640		
55	AAT GTT GGA AGC AGC AAC CGA AAC AAA GCT GAA AAC CTG TTG CGA GGG Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly		1920
	645	650	655
55	AAG CGA GAT GGC ACT TTT CTT GTC CGG GAG AGC AGT AAA CAG GGC TGC Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys		1968
	660	665	670
55	TAT GCC TGC TCT GTA GTG GTG GAC GGC GAA GTA AAG CAT TGT GTC ATA		2016

146

	Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys His Cys Val Ile		
	660	665	670
5	AAC AAA ACA GCA ACT GGC TAT GGC TTT GCC GAG CCC TAT AAC TTG TAC Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr		2064
	675	680	685
10	AGC TCT CTG AAA GAA CTG GTG CTA CAT TAC CAA CAC ACC TCC CTT GTG Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val		2112
	690	695	700
15	CAG CAC AAC GAC TCC CTC AAT GTC ACA CTA GCC TAC CCA GTA TAT GCA Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala		2160
	705	710	715
20	CAG CAG AGG CGA CAG GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC Gln Gln Arg Arg Gln Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly		2208
	725	730	735
25	GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly		2256
	740	745	750
30	GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp		2304
	755	760	765
35	GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys		2352
	770	775	780
40	CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val		2400
	785	790	795
45	CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe		2448
	805	810	815
50	AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe		2496
	820	825	830
55	AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly		2544
	835	840	845
60	GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu		2592
	850	855	860
65	GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His		2640
	865	870	875
70	AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC		2688

146

147

	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn			
	885	890	895	
5	TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC		2736	
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp			
	900	905	910	
10	CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC		2784	
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
	915	920	925	
15	GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC		2832	
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
	930	935	940	
20	GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG		2880	
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
	945	950	955	960
25	ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA		2913	
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
	965	970		

25 (2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys			
1	5	10	15
40 Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val			
20	25	30	
Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala			
35	40	45	
Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly			
50	55	60	
Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys			
65	70	75	80
Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro			
85	90	95	
50 Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala			
100	105	110	
Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala			
115	120	125	
Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu			
55 130	135	140	
Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Asn Leu Ala Glu			

	145	150	155	160
	Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met			
	165	170	175	
5	Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp			
	180	185	190	
	Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser			
	195	200	205	
	Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile Gln Leu Leu Lys			
	210	215	220	
10	Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr Trp Leu Thr Leu			
	225	230	235	240
	Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln Thr Ser Ser Lys			
	245	250	255	
	Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe Ser Pro Met Leu			
15	260	265	270	
	Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu Asn Leu Ile Lys			
	275	280	285	
	Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu Arg Gln Pro Ala			
	290	295	300	
20	Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn			
	305	310	315	320
	Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu Trp Tyr Trp Gly			
	325	330	335	
	Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp			
25	340	345	350	
	Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr			
	355	360	365	
	Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe			
	370	375	380	
30	His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser			
	385	390	395	400
	Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr			
	405	410	415	
	Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln			
35	420	425	430	
	Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys			
	435	440	445	
	Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp			
	450	455	460	
40	Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys			
	465	470	475	480
	Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu			
	485	490	495	
	Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe			
45	500	505	510	
	Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr			
	515	520	525	
	Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg			
	530	535	540	
50	Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp			
	545	550	555	560
	Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr			
	565	570	575	
	Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys			
55	580	585	590	
	Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser			

149

	595	600	605
	Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp		
	610	615	620
5	Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly		
	625	630	635
	Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys		640
	645	650	655
	Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys His Cys Val Ile		
	660	665	670
10	Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr		
	675	680	685
	Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val		
	690	695	700
15	Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala		
	705	710	715
	Gln Gln Arg Arg Gln Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly		720
	725	730	735
	Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly		
	740	745	750
20	Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp		
	755	760	765
	Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys		
	770	775	780
25	Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val		
	785	790	795
	Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe		800
	805	810	815
	Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe		
	820	825	830
30	Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly		
	835	840	845
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu		
	850	855	860
35	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His		
	865	870	875
	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn		880
	885	890	895
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp		
	900	905	910
40	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro		
	915	920	925
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn		
	930	935	940
45	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly		
	945	950	955
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		960
	965	970	

(2) INFORMATION FOR SEQ ID NO:68:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

150

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

5 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1785
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

10	ATG GGC AAC GCC GCC GCC AAG AAG GGC AGC GAG CAG AGC GTG Met Gly Asn Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val 1 5 10 15	48
15	AAA GAG TTC CTA GCC AAA GCC AAG GAA GAT TTC CTG AAA AAA TGG GAA Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu 20 25 30	96
20	GAC CCC TCT CAG AAT ACA GCC CAG TTG GAT CAG TTT GAT AGA ATC AAG Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys 35 40 45	144
25	ACC CTT GGC ACC GGC TCC TTT GGG CGA GTG ATG CTG GTG AAG CAC AAG Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys 50 55 60	192
30	GAG AGT GGG AAC CAC TAC GCC ATG AAG ATC TTA GAC AAG CAG AAG GTG Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val 65 70 75 80	240
35	GTG AAG CTA AAG CAG ATC GAG CAC ACT CTG AAT GAG AAG CGC ATC CTG Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu 85 90 95	288
40	CAG GCC GTC AAC TTC CCG TTC CTG GTC AAA CTT GAA TTC TCC TTC AAG Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys 100 105 110	336
45	GAC AAC TCA AAC CTG TAC ATG GTC ATG GAG TAT GTA GCT GGT GGC GAG Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Ala Gly Gly Glu 115 120 125	384
50	ATG TTC TCC CAC CTA CGG CGG ATT GGA AGG TTC AGC GAG CCC CAT GCC Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala 130 135 140	432
55	CGT TTC TAC GCG GCG CAG ATC GTC CTG ACC TTT GAG TAT CTG CAC TCC Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser 145 150 155 160	480
60	CTG GAC CTC ATC TAC CGG GAC CTG AAG CCC GAG AAT CTT CTC ATC GAC Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp 165 170 175	528
65	CAG CAG GGC TAT ATT CAG GTG ACA GAC TTC GGT TTT GCC AAG CGT GTG Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val 180 185 190	576

	AAA GGC CGT ACT TGG ACC TTG TGT GGG ACC CCT GAG TAC TTG GCC CCC Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro 195 200 205	624
5	GAG ATT ATC CTG AGC AAA GGC TAC AAC AAG GCT GTG GAC TGG TGG GCT Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala 210 215 220	672
10	CTC GGA GTC CTC ATC TAC GAG ATG GCT GCT GGT TAC CCA CCC TTC TTC Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe 225 230 235 240	720
15	GCT GAC CAG CCT ATC CAG ATC TAT GAG AAA ATC GTC TCT GGG AAG GTG Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val 245 250 255	768
20	CGG TTC CCA TCC CAC TTC AGC TCT GAC TTG AAG GAC CTG CTG CGG AAC Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn 260 265 270	816
25	CTT CTG CAA GTG GAT CTA ACC AAG CGC TTT GGA AAC CTC AAG GAC GGG Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly 275 280 285	864
30	GTC AAT GAC ATC AAG AAC CAC AAG TGG TTT GCC ACG ACT GAC TGG ATT Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile 290 295 300	912
35	GCC ATC TAT CAG AGA AAG GTG GAA GCT CCC TTC ATA CCA AAG TTT AAA Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys 305 310 315 320	960
40	GGC CCT GGG GAC ACG AGT AAC TTT GAC GAC TAT GAG GAG GAA GAG ATC Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Ile 325 330 335	1008
45	CGG GTC TCC ATC AAT GAG AAG TGT GGC AAG GAG TTT ACT GAG TTT GGG Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly 340 345 350	1056
50	CGC GCC ATG AGT AAA GGA GAA CTT TTC ACT GGA GTT GTC CCA ATT Arg Ala Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile 355 360 365	1104
55	CTT GTT GAA TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT AGT Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser 370 375 380	1152
	GGA GAG GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 385 390 395 400	1200
	ATT TGC ACT ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC ACT Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 405 410 415	1248

152

	ACT CTC ACT TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT ATG Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met 420 425 430	1296
5	AAA CAG CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 435 440 445	1344
10	GAA AGA ACT ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 450 455 460	1392
15	GAA GTC AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 465 470 475 480	1440
20	GGT ATT GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG GAA Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu 485 490 495	1488
25	TAC AAT TAT AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA AAG Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys 500 505 510	1536
30	AAT GGC ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT GGA Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly 515 520 525	1584
35	AGC GTT CAA TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 530 535 540	1632
40	GGC CCT GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT GCC Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 545 550 555 560	1680
45	CTT TCC AAA GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT GAG Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu 565 570 575	1728
50	TTT GTA ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 580 585 590	1776
	CCT CAG GAG TAA Pro Gln Glu 595	1788
	(2) INFORMATION FOR SEQ ID NO:69:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 595 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single	
55		152

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

	Met	Gly	Asn	Ala	Ala	Ala	Ala	Lys	Gly	Ser	Glu	Gln	Glu	Ser	Val	
1	1	5						10						15		
10	Lys	Glu	Phe	Leu	Ala	Lys	Ala	Lys	Glu	Asp	Phe	Leu	Lys	Lys	Trp	Glu
								20				25		30		
	Asp	Pro	Ser	Gln	Asn	Thr	Ala	Gln	Leu	Asp	Gln	Phe	Asp	Arg	Ile	Lys
								35			40		45			
15	Thr	Leu	Gly	Thr	Gly	Ser	Phe	Gly	Arg	Val	Met	Leu	Val	Lys	His	Lys
								50			55		60			
	Glu	Ser	Gly	Asn	His	Tyr	Ala	Met	Lys	Ile	Leu	Asp	Lys	Gln	Lys	Val
								65			70		75		80	
	Val	Lys	Leu	Lys	Gln	Ile	Glu	His	Thr	Leu	Asn	Glu	Lys	Arg	Ile	Leu
								85			90		95			
20	Gln	Ala	Val	Asn	Phe	Pro	Phe	Leu	Val	Lys	Leu	Glu	Phe	Ser	Phe	Lys
								100			105		110			
	Asp	Asn	Ser	Asn	Leu	Tyr	Met	Val	Met	Glu	Tyr	Val	Ala	Gly	Gly	Glu
								115			120		125			
25	Met	Phe	Ser	His	Leu	Arg	Arg	Ile	Gly	Arg	Phe	Ser	Glu	Pro	His	Ala
								130			135		140			
	Arg	Phe	Tyr	Ala	Ala	Gln	Ile	Val	Leu	Thr	Phe	Glu	Tyr	Leu	His	Ser
								145			150		155		160	
	Leu	Asp	Leu	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Ile	Asp
								165			170		175			
30	Gln	Gln	Gly	Tyr	Ile	Gln	Val	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Arg	Val
								180			185		190			
	Lys	Gly	Arg	Thr	Trp	Thr	Leu	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro
								195			200		205			
35	Glu	Ile	Ile	Leu	Ser	Lys	Gly	Tyr	Asn	Lys	Ala	Val	Asp	Trp	Trp	Ala
								210			215		220			
	Leu	Gly	Val	Leu	Ile	Tyr	Glu	Met	Ala	Ala	Gly	Tyr	Pro	Pro	Phe	Phe
								225			230		235		240	
	Ala	Asp	Gln	Pro	Ile	Gln	Ile	Tyr	Glu	Lys	Ile	Val	Ser	Gly	Lys	Val
								245			250		255			
40	Arg	Phe	Pro	Ser	His	Phe	Ser	Ser	Asp	Leu	Lys	Asp	Leu	Leu	Arg	Asn
								260			265		270			
	Leu	Leu	Gln	Val	Asp	Leu	Thr	Lys	Arg	Phe	Gly	Asn	Leu	Lys	Asp	Gly
								275			280		285			
45	Val	Asn	Asp	Ile	Lys	Asn	His	Lys	Trp	Phe	Ala	Thr	Thr	Asp	Trp	Ile
								290			295		300			
	Ala	Ile	Tyr	Gln	Arg	Lys	Val	Glu	Ala	Pro	Phe	Ile	Pro	Lys	Phe	Lys
								305			310		315		320	
	Gly	Pro	Gly	Asp	Thr	Ser	Asn	Phe	Asp	Asp	Tyr	Glu	Glu	Glu	Ile	
								325			330		335			
50	Arg	Val	Ser	Ile	Asn	Glu	Lys	Cys	Gly	Lys	Glu	Phe	Thr	Glu	Phe	Gly
								340			345		350			
	Arg	Ala	Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile
								355			360		365			
55	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser
								370			375		380			
	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe

154

	385	390	395	400
	Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
	405	410	415	
5	Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
	420	425	430	
	Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
	435	440	445	
10	Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
	450	455	460	
	Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
	465	470	475	480
	Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu			
	485	490	495	
15	Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys			
	500	505	510	
	Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly			
	515	520	525	
	Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
	530	535	540	
20	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
	545	550	555	560
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu			
	565	570	575	
25	Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys			
	580	585	590	
	Pro Gln Glu			
	595			

(2) INFORMATION FOR SEQ ID NO:70:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2178

(D) OTHER INFORMATION:

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATG	AGC	GAC	GTG	GCT	ATT	GTG	AAG	GAG	GGT	TGG	CTG	CAC	AAA	CGA	GGG
Met	Ser	Asp	Val	Ala	Ile	Val	Lys	Glu	Gly	Trp	Leu	His	Lys	Arg	Gly
1					5					10				15	

48

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GAG	TAC	ATC	AAG	ACC	TGG	CGG	CCA	CCG	TAC	TTC	CTC	CTC	AAG	AAT	GAT
Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	Tyr	Phe	Leu	Leu	Lys	Asn	Asp
20					25								30		

96

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GGC	ACC	TTC	ATT	GGC	TAC	AAG	GAG	CGG	CCG	CAG	GAT	GTG	GAC	CAA	CGT
Gly	Thr	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	Pro	Gln	Asp	Val	Asp	Gln	Arg
35						40				45					

144

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	GAG GCT CCC CTC AAC AAC TTC TCT GTG GCG CAG TGC CAG CTG ATG AAG Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys 50 55 60	192
5	ACG GAG CGG CCC CGG CCC AAC ACC TTC ATC ATC CGC TGC CTG CAG TGG Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp 65 70 75 80	240
10	ACC ACT GTC ATC GAA CGC ACC TTC CAT GTG GAG ACT CCT GAG GAG CGG Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg 85 90 95	288
15	GAG GAG TGG ACA ACC GCC ATC CAG ACT GTG GCT GAC GGC CTC AAG AAG Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys 100 105 110	336
20	CAG GAG GAG GAG ATG GAC TTC CGG TCG GGC TCA CCC AGT GAC AAC Gln Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn 115 120 125	384
25	TCA GGG GCT GAA GAG ATG GAG GTG TCC CTG GCC AAG CCC AAG CAC CGC Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg 130 135 140	432
30	GTG ACC ATG AAC GAG TTT GAG TAC CTG AAG CTG CTG GGC AAG GGC ACT Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr 145 150 155 160	480
35	TTC GGC AAG GTG ATC CTG GTG AAG GAG AAG GCC ACA GCA GGC CGC TAC TAC Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr 165 170 175	528
40	GCC ATG AAG ATC CTC AAG AAG GAA GTC ATC GTG GCC AAG GAC GAG GTG Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val 180 185 190	576
45	GCC CAC ACA CTC ACC GAG AAC CGC GTC CTG CAG AAC TCC AGG CAC CCC Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro 195 200 205	624
50	TTC CTC ACA GCC CTG AAG TAC TCT TTC CAG ACC CAC GAC CGC CTC TGC Phe Leu Thr Ala Leu Lys Tyr Ser Phe Glu Lys Thr His Asp Arg Leu Cys 210 215 220	672
55	TTT GTC ATG GAG TAC GCC AAC GGG GGC GAG CTG TTC TTC CAC CTG TCC Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser 225 230 235 240	720
50	CGG GAA CGT GTG TTC TCC GAG GAC CGG GCC CGC TTC TAT GGC GCT GAG Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu 245 250 255	768
55	ATT GTG TCA GCC CTG GAC TAC CTG CAC TCG GAG AAG AAC GTG GTG TAC Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr 260 265 270	816

156

	CGG GAC CTC AAG CTG GAG AAC CTC ATG CTG GAC AAG GAC GGG CAC ATT		864
Arg	Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile		
5	275	280	285
	AAG ATC ACA GAC TTC GGG CTG TGC AAG GAG GGG ATC AAG GAC GGT GCC		912
Lys	Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala		
	290	295	300
10	ACC ATG AAG ACC TTT TGC GGC ACA CCT GAG TAC CTG GCC CCC GAG GTG		960
Thr	Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val		
	305	310	315
	320		
15	CTG GAG GAC AAT GAC TAC GGC CGT GCA GTG GAC TGG TGG GGG CTG GGC		1008
Leu	Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly		
	325	330	335
20	GTG GTC ATG TAC GAG ATG ATG TGC GGT CGC CTG CCC TTC TAC AAC CAG		1056
Val	Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln		
	340	345	350
	350		
	GAC CAT GAG AAG CTT TTT GAG CTC ATC CTC ATG GAG GAG ATC CGC TTC		1104
Asp	His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe		
	355	360	365
25	CCG CGC ACG CTT GGT CCC GAG GCC AAG TCC TTG CTT TCA GGG CTG CTC		1152
Pro	Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu		
	370	375	380
30	AAG AAG GAC CCC AAG CAG AGG CTT GGC GGG GGC TCC GAG GAC GCC AAG		1200
Lys	Lys Asp Pro Lys Gln Arg Leu Gly Gly Ser Glu Asp Ala Lys		
	385	390	395
	400		
35	GAG ATC ATG CAG CAT CGC TTC TTT GCC GGT ATC GTG TGG CAG CAC GTG		1248
Glu	Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val		
	405	410	415
40	TAC GAG AAG CTC AGC CCA CCC TTC AAG CCC CAG GTC ACG TCG GAG		1296
Tyr	Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu		
	420	425	430
	430		
	ACT GAC ACC AGG TAT TTT GAT GAG GAG TTC ACG GCC CAG ATG ATC ACC		1344
Thr	Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr		
	435	440	445
45	ATC ACA CCA CCT GAC CAA GAT GAC AGC ATG GAG TGT GTG GAC AGC GAG		1392
Ile	Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu		
	450	455	460
50	CGC AGG CCC CAC TTC CCC CAG TTC TCC TAC TCG GCC AGC AGC ACG GCC		1440
Arg	Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala		
	465	470	475
	480		
55	TCG GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC		1488
Ser	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe		
	485	490	495
	495		

157

	ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly 500 505 510	1536
5	CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC His Lys Phe Ser Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly 515 520 525	1584
10	AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro 530 535 540	1632
15	TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser 545 550 555 560	1680
20	CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met 565 570 575	1728
25	CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly 580 585 590	1776
30	AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val 595 600 605	1824
35	AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile 610 615 620	1872
40	CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile 625 630 635 640	1920
45	ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg 645 650 655	1968
50	CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln 660 665 670	2016
55	AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr 675 680 685	2064
50	CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp 690 695 700	2112
55	CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GGC GGG ATC ACT CTC GGC His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly 705 710 715 720	2160

157

ATG GAC GAG CTG TAC AAG TAA
 Met Asp Glu Leu Tyr Lys
 725

2181

5

(2) INFORMATION FOR SEQ ID NO:71:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 726 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

20 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
 1 5 10 15
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
 20 25 30
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
 25 35 40 45
 Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
 30 50 55 60
 Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
 35 65 70 75 80
 30 Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
 40 85 90 95
 Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys
 45 100 105 110
 Gln Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
 50 115 120 125
 Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg
 55 130 135 140
 Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
 60 145 150 155 160
 40 Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr
 65 165 170 175
 Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val
 70 180 185 190
 Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro
 75 195 200 205
 Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys
 80 210 215 220
 Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser
 85 225 230 235 240
 50 Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu
 90 245 250 255
 Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr
 95 260 265 270
 Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile
 100 275 280 285
 Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala

159

	290	295	300
	Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val		
	305	310	315
5	Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly		320
	325	330	335
	Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln		
	340	345	350
	Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe		
	355	360	365
10	Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu		
	370	375	380
	Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Ser Glu Asp Ala Lys		
	385	390	395
	Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val		400
15	405	410	415
	Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu		
	420	425	430
	Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr		
	435	440	445
20	Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu		
	450	455	460
	Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala		
	465	470	475
	Ser Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe		480
25	485	490	495
	Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly		
	500	505	510
	His Lys Phe Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly		
	515	520	525
30	Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro		
	530	535	540
	Trp Pro Thr Leu Val Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser		
	545	550	555
	Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met		560
35	565	570	575
	Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly		
	580	585	590
	Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val		
	595	600	605
40	Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile		
	610	615	620
	Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile		
	625	630	635
	Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg		640
45	645	650	655
	His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln		
	660	665	670
	Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr		
	675	680	685
50	Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp		
	690	695	700
	His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly		
	705	710	715
	Met Asp Glu Leu Tyr Lys		720
55	725		

159

160

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (ix) FEATURE:

- 15 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2748
 (D) OTHER INFORMATION:

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

	ATG GCT GAC GTT TAC CCG GCC AAC GAC TCC ACG GCG TCT CAG GAC GTG	48
20	Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val	
	1 5 10 15	
	GCC AAC CGC TTC GCC CGC AAA GGG GCG CTG AGG CAG AAG AAC GTG CAT	96
25	Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His	
	20 25 30	
	GAG GTG AAA GAC CAC AAA TTC ATC GCC CGC TTC TTC AAG CAA CCC ACC	144
30	Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr	
	35 40 45	
	TTC TGC AGC CAC TGC ACC GAC TTC ATC TGG GGG TTT GGG AAA CAA GGC	192
35	Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly	
	50 55 60	
	TTC CAG TGC CAA GTT TGC TGT TTT GTG GTT CAT AAG AGG TGC CAT GAG	240
40	Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu	
	65 70 75 80	
	TTC GTT ACG TTC TCT TGT CCG GGT GCG GAT AAG GGA CCT GAC ACT GAC	288
45	Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp	
	85 90 95	
	GAC CCC AGG AGC AAG CAC AAG TTC AAA ATC CAC ACA TAC GGA AGC CCT	336
50	Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro	
	100 105 110	
	ACC TTC TGT GAT CAC TGT GGG TCC CTG CTC TAT GGA CTT ATC CAC CAA	384
55	Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln	
	115 120 125	
	GGG ATG AAA TGT GAC ACC TGC GAC ATG AAT GTT CAC AAC CAG TGT GTG	432
60	Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val	
	130 135 140	
	ATC AAT GAC CCT AGC CTC TGC GGA ATG GAT CAC ACA GAG AAG AGG GGG	480
65	Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly	
	145 150 155 160	

160

161

	CGG ATT TAT CTG AAG GCT GAG GTC ACT GAT GAA AAG CTC CAC GTC ACG Arg Ile Tyr Leu Lys Ala Glu Val Thr Asp Glu Lys Leu His Val Thr	528
5	165 170 175	
	GTA CGA GAT GCA AAA AAT CTA ATC CCT ATG GAT CCA AAT GGG CTT TCG Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser	576
	180 185 190	
10	GAT CCT TAT GTG AAG CTG AAA CTA ATC CCT GAC CCC AAG AAT GAG AGC Asp Pro Tyr Val Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser	624
	195 200 205	
15	AAA CAG AAA ACC AAA ACC ATC CGC TCC AAC CTG AAT CCT CAG TGG AAT Lys Gln Lys Thr Lys Thr Ile Arg Ser Asn Leu Asn Pro Gln Trp Asn	672
	210 215 220	
20	GAG TCC TTC ACG TTC AAA TTA AAA CCT TCA GAC AAA GAC CGG CGA CTG Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu	720
	225 230 235 240	
	TCT GTA GAA ATC TGG GAC TGG GAT CGG ACG ACT CGG AAT GAC TTC ATG Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met	768
	245 250 255	
25	GGA TCC CTT TCC TTT GGT GTC TCA GAG CTA ATG AAG ATG CCG GCC AGT Gly Ser Leu Ser Phe Gly Val Ser Glu Leu Met Lys Met Pro Ala Ser	816
	260 265 270	
30	GGA TGG TAT AAA GCT CAC AAC CAA GAA GAG GGC GAA TAT TAC AAC GTG Gly Trp Tyr Lys Ala His Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val	864
	275 280 285	
35	CCC ATT CCA GAA GGA GAT GAA GAA GGC AAC ATG GAA CTC AGG CAG AAG Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys	912
	290 295 300	
40	TTT GAG AAA GCC AAG CTA GGT CCT GTT GGT AAC AAA GTC ATC AGC CCT Phe Glu Lys Ala Lys Leu Gly Pro Val Gly Asn Lys Val Ile Ser Pro	960
	305 310 315 320	
	TCA GAA GAC AGA AAG CAA CCA TCC AAC AAC CTG GAC AGA GTG AAA CTC Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu	1008
	325 330 335	
45	ACA GAC TTC AAC TTC CTC ATG GTG CTG GGG AAG GGG AGT TTT GGG AAG Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys	1056
	340 345 350	
50	GTG ATG CTT GCT GAC AGG AAG GGA ACG GAG GAA CTG TAC GCC ATC AAG Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys	1104
	355 360 365	
55	ATC CTG AAG AAG GAC GTG GTG ATC CAG GAC GAC GTG GAG TGC ACC Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr	1152
	370 375 380	

161

162

	ATG GTG GAG AAG CGC GTG CTG GCC CTG CTG GAC AAG CCG CCA TTT CTG Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu 385 390 395 400	1200
5	ACA CAG CTG CAC TCC TGC TTC CAG ACA GTG GAC CGG CTG TAC TTC GTC Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val 405 410 415	1248
10	ATG GAA TAC GTC AAC GGC GGG GAT CTT ATG TAC CAC ATT CAG CAA GTC Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val 420 425 430	1296
15	GGG AAA TTT AAG GAG CCA CAA GCA GTA TTC TAC GCA GCC GAG ATC TCC Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser 435 440 445	1344
20	ATC GGA CTG TTC CTT CAT AAA AGA GGG ATC ATT TAC AGG GAT CTG Ile Gly Leu Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu 450 455 460	1392
25	AAG CTG AAC AAT GTC ATG CTG AAC TCA GAA GGG CAC ATC AAA ATC GCC Lys Leu Asn Asn Val Met Leu Asn Ser Glu Gly His Ile Lys Ile Ala 465 470 475 480	1440
30	GAC TTC GGG ATG TGC AAG GAA CAC ATG ATG GAT GGA GTC ACG ACC AGG Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg 485 490 495	1488
35	ACC TTC TGC GGA ACT CCG GAC TAC ATT GCC CCA GAG ATA ATC GCT TAC Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr 500 505 510	1536
40	CAG CCG TAC GGG AAG TCT GTA GAT TGG TGG GCG TAC GGT GTG CTG CTG Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu 515 520 525	1584
45	TAC GAG ATG CTA GCC GGG CAG CCT CCG TTT GAT GGT GAA GAT GAA GAT Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp 530 535 540	1632
50	GAA CTG TTT CAG TCT ATA ATG GAG CAC AAC GTG TCC TAC CCC AAA TCC Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser 545 550 555 560	1680
55	TTG TCC AAG GAA GCC GTC TCC ATC TGC AAA GGA CTT ATG ACC AAA CAG Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys Gln 565 570 575	1728
580 585 590		1776
595 600 605		1824

162

163

	GAG ATC CAA CCA CCA TTC AAG CCC AAA GTG TGT GGC AAA GGA GCA GAA Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu 610 615 620	1872
5	AAC TTT GAC AAG TTC TTC ACG CGA GGA CAG CCT GTC TTA ACA CCA CCA Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro 625 630 635 640	1920
10	GAT CAG CTG GTC ATT GCT AAC ATA GAC CAA TCT GAT TTT GAA GGG TTC Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe 645 650 655	1968
15	TCG TAT GTC AAC CCC CAG TTT GTG CAC CCA ATC TTG CAA AGT GCA GTA Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val 660 665 670	2016
20	GGG CGC GCC ATG AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA Gly Arg Ala Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro 675 680 685	2064
	ATT CTT GTT GAA TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val 690 695 700	2112
25	AGT GGA GAG GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 705 710 715 720	2160
30	TTT ATT TGC ACT ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val 725 730 735	2208
35	ACT ACT CTC ACT TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His 740 745 750	2256
	ATG AAA CAG CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val	2304
40	755 760 765	
	CAG GAA AGA ACT ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg 770 775 780	2352
45	GCT GAA GTC AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 785 790 795 800	2400
50	AAA GGT ATT GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met 805 810 815	2448
	GAA TAC AAT TAT AAC TCA CAT AAT GTC TAC ATC ATG GCA GAC AAA CCA Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro 820 825 830	2496

164

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 916 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

		1	5	10	15
	Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His				
	20	25		30	
45	Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr				
	35	40	45		
	Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly				
	50	55	60		
	Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu				
	65	70	75	80	
50	Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp				
	85	90	95		
	Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro				
	100	105	110		
55	Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln				
	115	120	125		
	Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val				

165

	130	135	140
	Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly		
	145	150	155
5	Arg Ile Tyr Leu Lys Ala Glu Val Thr Asp Glu Lys Leu His Val Thr		160
	165	170	175
	Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser		
	180	185	190
	Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser		
	195	200	205
10	Lys Gln Lys Thr Lys Thr Ile Arg Ser Asn Leu Asn Pro Gln Trp Asn		
	210	215	220
	Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu		
	225	230	235
	Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met		240
15	245	250	255
	Gly Ser Leu Ser Phe Gly Val Ser Glu Leu Met Lys Met Pro Ala Ser		
	260	265	270
	Gly Trp Tyr Lys Ala His Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val		
	275	280	285
20	Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys		
	290	295	300
	Phe Glu Lys Ala Lys Leu Gly Pro Val Gly Asn Lys Val Ile Ser Pro		
	305	310	315
	Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu		320
25	325	330	335
	Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys		
	340	345	350
	Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys		
	355	360	365
30	Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr		
	370	375	380
	Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu		
	385	390	395
	Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val		400
35	405	410	415
	Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val		
	420	425	430
	Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser		
	435	440	445
40	Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu		
	450	455	460
	Lys Leu Asn Asn Val Met Leu Asn Ser Glu Gly His Ile Lys Ile Ala		
	465	470	475
	Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg		480
45	485	490	495
	Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr		
	500	505	510
	Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu		
	515	520	525
50	Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp		
	530	535	540
	Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser		
	545	550	555
	Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys Gln		560
55	565	570	575
	Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg		

166

	580	585	590
	Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg		
	595	600	605
5	Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu		
	610	615	620
	Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro		
	625	630	635
	Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe		
	645	650	655
10	Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val		
	660	665	670
	Gly Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
	675	680	685
15	Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val		
	690	695	700
	Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
	705	710	715
	Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
	725	730	735
20	Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His		
	740	745	750
	Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
	755	760	765
	Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg		
25	770	775	780
	Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu		
	785	790	795
	Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met		
	805	810	815
30	Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro		
	820	825	830
	Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp		
	835	840	845
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
35	850	855	860
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
	865	870	875
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu		
	885	890	895
40	Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr		
	900	905	910
	Lys Pro Gln Glu		
	915		

45 (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 55 (A) NAME/KEY: Coding Sequence

167

(B) LOCATION: 1...2154
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

5	ATG TCG TCC ATC TTG CCA TTC ACG CCG CCA GTT GTG AAG AGA CTG CTG Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu 1 5 10 15	48
10	GGA TGG AAG AAG TCA GCT GGT GGG TCT GGA GGA GCA GGC GGA GGA GAG Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Glu 20 25 30	96
15	CAG AAT GGG CAG GAA GAA AAG TGG TGT GAG AAA GCA GTG AAA AGT CTG Gln Asn Gly Gln Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu 35 40 45	144
20	GTG AAG AAG CTA AAG AAA ACA GGA CGA TTA GAT GAG CTT GAG AAA GCC Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala 50 55 60	192
25	ATC ACC ACT CAA AAC TGT AAT ACT AAA TGT GTT ACC ATA CCA AGC ACT Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr 65 70 75 80	240
30	TGC TCT GAA ATT TGG GGA CTG AGT ACA CCA AAT ACG ATA GAT CAG TGG Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp 85 90 95	288
35	GAT ACA ACA GGC CTT TAC AGC TTC TCT GAA CAA ACC AGG TCT CTT GAT Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp 100 105 110	336
40	GGT CGT CTC CAG GTA TCC CAT CGA AAA GGA TTG CCA CAT GTT ATA TAT Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr 115 120 125	384
45	TGC CGA TTA TGG CGC TGG CCT GAT CTT CAC AGT CAT CAT GAA CTC AAG Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys 130 135 140	432
50	GCA ATT GAA AAC TGC GAA TAT GCT TTT AAT CTT AAA AAG GAT GAA GTA Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val 145 150 155 160	480
55	TGT GTA AAC CCT TAC CAC TAT CAG AGA GTT GAG ACA CCA GTT TTG CCT Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro 165 170 175	528
55	CCA GTA TTA GTG CCC CGA CAC ACC GAG ATC CTA ACA GAA CTT CCG CCT Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro 180 185 190	576
55	CTG GAT GAC TAT ACT CAC TCC ATT CCA GAA AAC ACT AAC TTC CCA GCA Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala 195 200 205	624

167

168

	GGA ATT GAG CCA CAG AGT AAT TAT ATT CCA GAA ACG CCA CCT CCT GGA Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly 210 215 220	672
5	TAT ATC AGT GAA GAT GGA GAA ACA AGT GAC CAA CAG TTG AAT CAA AGT Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser 225 230 235 240	720
10	ATG GAC ACA GGC TCT CCA GCA GAA CTA TCT CCT ACT ACT CTT TCC CCT Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro 245 250 255	768
15	GTT AAT CAT AGC TTG GAT TTA CAG CCA GTT ACT TAC TCA GAA CCT GCA Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala 260 265 270	816
20	TTT TGG TGT TCA ATA GCA TAT TAT GAA TTA AAT CAG AGG GTT GGA GAA Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu 275 280 285	864
25	ACC TTC CAT GCA TCA CAG CCC TCA CTC ACT GTA GAT GGC TTT ACA GAC Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp 290 295 300	912
30	CCA TCA AAT TCA GAG AGG TTC TGC TTA GGT TTA CTC TCC AAT GTT AAC Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn 305 310 315 320	960
35	CGA AAT GCC ACG GTA GAA ATG ACA AGA AGG CAT ATA GGA AGA GGA GTG Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val 325 330 335	1008
40	CGC TTA TAC TAC ATA GGT GGG GAA GTT TTT GCT GAG TGC CTA AGT GAT Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp 340 345 350	1056
45	AGT GCA ATC TTT GTG CAG AGC CCC AAT TGT AAT CAG AGA TAT GGC TGG Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp 355 360 365	1104
50	CAC CCT GCA ACA GTG TGT AAA ATT CCA CCA GGC TGT AAT CTG AAG ATC His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile 370 375 380	1152
55	TTC AAC AAC CAG GAA TTT GCT CTT CTG GCT CAG TCT GTT AAT CAG phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln 385 390 395 400	1200
	GGT TTT GAA GCC GTC TAT CAG CTA ACT AGA ATG TGC ACC ATA AGA ATG Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met 405 410 415	1248
	AGT TTT GTG AAA GGG TGG GGA GCA GAA TAC CGA AGG CAG ACG GTA ACA Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr 420 425 430	1296

168

169

	AGT ACT CCT TGC TGG ATT GAA CTT CAT CTG AAT GGA CCT CTA CAG TGG Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp 435 440 445	1344
5	TTG GAC AAA GTA TTA ACT CAG ATG GGA TCC CCT TCA GTG CGT TGC TCA Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser 450 455 460	1392
10	AGC ATG TCA TGG GTA CCG CGG GCC CGG GAT CCA CCG GTC GCC ACC ATG Ser Met Ser Trp Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met 465 470 475 480	1440
15	GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 485 490 495	1488
20	GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 500 505 510	1536
25	GCC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 515 520 525	1584
30	ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 530 535 540	1632
35	ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln 545 550 555 560	1680
40	CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 565 570 575	1728
45	ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 580 585 590	1776
50	AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 595 600 605	1824
55	GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 610 615 620	1872
50	TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAC GGC Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 625 630 635 640	1920
55	ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 645 650 655	1968

170

	CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 660 665 670	2016
5	GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser 675 680 685	2064
10	AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 690 695 700	2112
15	ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 705 710 715	2157

(2) INFORMATION FOR SEQ ID NO:75:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

	Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu 1 5 10 15
35	Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu 20 25 30
	Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu 35 40 45
40	Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala 50 55 60
	Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr 65 70 75 80
45	Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp 85 90 95
	Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp 100 105 110
50	Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr 115 120 125
	Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys 130 135 140
55	Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val 145 150 155 160
	Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro 165 170 175
	Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro 180 185 190
	Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala

170

	195	200	205
	Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly		
	210	215	220
5	Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser		
	225	230	235
	Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro		240
	245	250	255
	Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala		
	260	265	270
10	Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu		
	275	280	285
	Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp		
	290	295	300
	Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn		
15	305	310	315
	Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val		320
	325	330	335
	Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp		
	340	345	350
20	Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp		
	355	360	365
	His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile		
	370	375	380
	Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln		
25	385	390	395
	Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met		400
	405	410	415
	Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr		
	420	425	430
30	Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp		
	435	440	445
	Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser		
	450	455	460
	Ser Met Ser Trp Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met		
35	465	470	475
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		480
	485	490	495
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
	500	505	510
40	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
	515	520	525
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
	530	535	540
	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		
45	545	550	555
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		560
	565	570	575
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
	580	585	590
50	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
	595	600	605
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
	610	615	620
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
55	625	630	635
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		640

172

	645	650	655													
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
	660															670
	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
5	675															685
	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	690															700
	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
	705															

10 (2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 2397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2394
 (D) OTHER INFORMATION:

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

	ATG	GAC	AAT	ATG	TCT	ATT	ACG	AAT	ACA	CCA	ACA	AGT	AAT	GAT	GCC	TGT	48
	Met	Asp	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys	
30	1			5					10							15	
	CTG	AGC	ATT	GTG	CAT	AGT	TTG	ATG	TGC	CAT	AGA	CAA	GGT	GGA	GAG	AGT	96
	Leu	Ser	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser	
				20					25							30	
35	GAA	ACA	TTT	GCA	AAA	AGA	GCA	ATT	GAA	AGT	TTG	GTA	AAG	AAG	CTG	AAG	144
	Glu	Thr	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys	
				35					40							45	
40	GAG	AAA	AAA	GAT	GAA	TTG	GAT	TCT	TTA	ATA	ACA	GCT	ATA	ACT	ACA	AAT	192
	Glu	Lys	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn	
				50					55							60	
45	GGA	GCT	CAT	CCT	AGT	AAA	TGT	GTT	ACC	ATA	CAG	AGA	ACA	TTG	GAT	GGG	240
	Gly	Ala	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly	
				65					70							80	
50	AGG	CTT	CAG	GTG	GCT	GGT	CGG	AAA	GGA	TTT	CCT	CAT	GTG	ATC	TAT	GCC	288
	Arg	Leu	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala	
				85					90							95	
55	CGT	CTC	TGG	AGG	TGG	CCT	GAT	CTT	CAC	AAA	AAT	GAA	CTA	AAA	CAT	GTT	336
	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val	
				100					105							110	
	AAA	TAT	TGT	CAG	TAT	GCG	TTT	GAC	TTA	AAA	TGT	GAT	AGT	GTC	TGT	GTG	384

172

173

	Lys Tyr Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val		
	115	120	125
5	AAT CCA TAT CAC TAC GAA CGA GTT GTA TCA CCT GGA ATT GAT CTC TCA Asn Pro Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser		432
	130	135	140
10	GGA TTA ACA CTG CAG AGT AAT GCT CCA TCA AGT ATG ATG GTG AAG GAT Gly Leu Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp		480
	145	150	155
	160		
15	GAA TAT GTG CAT GAC TTT GAG GGA CAG CCA TCG TTG TCC ACT GAA GGA Glu Tyr Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly		528
	165	170	175
20	CAT TCA ATT CAA ACC ATC CAG CAT CCA CCA AGT AAT CGT GCA TCG ACA His Ser Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr		576
	180	185	190
25	GAG ACA TAC AGC ACC CCA GCT CTG TTA GCC CCA TCT GAG TCT AAT GCT Glu Thr Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala		624
	195	200	205
30	ACC AGC ACT GCC AAC TTT CCC AAC ATT CCT GTG GCT TCC ACA AGT CAG Thr Ser Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln		672
	210	215	220
35	CCT GCC AGT ATA CTG GGG GGC AGC CAT AGT GAA GGA CTG TTG CAG ATA Pro Ala Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile		720
	225	230	235
	240		
40	245	250	255
45	GCA TCA GGG CCT CAG CCA GGA CAG CAG CAG AAT GGA TTT ACT GGT CAG Ala Ser Gly Pro Gln Pro Gly Gln Gln Asn Gly Phe Thr Gly Gln		768
	260	265	270
50	CCA GCT ACT TAC CAT AAC AGC ACT ACC ACC TGG ACT GGA AGT AGG Pro Ala Thr Tyr His His Asn Ser Thr Thr Trp Thr Gly Ser Arg		816
	275	280	285
55	ACT GCA CCA TAC ACA CCT AAT TTG CCT CAC CAC CAA AAC GGC CAT CTT Thr Ala Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu		864
	290	295	300
60	CAG CAC CAC CCG CCT ATG CCG CCC CAT CCC GGA CAT TAC TGG CCT GTT Gln His His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val		912
	305	310	315
	320		
65	CAC AAT GAG CTT GCA TTC CAG CCT CCC ATT TCC AAT CAT CCT GCT CCT His Asn Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro		960
	325	330	335
70	GAG TAT TGG TGT TCC ATT GCT TAC TTT GAA ATG GAT GTT CAG GTA GGA Glu Tyr Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly		1008
	340	345	350
75	GAG ACA TTT AAG GTT CCT TCA AGC TGC CCT ATT GTT ACT GTT GAT GGA		1056

174

	Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly		
	340	345	350
5	TAC GTG GAC CCT TCT GGA GGA GAT CGC TTT TGT TTG GGT CAA CTC TCC Tyr Val Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser		1104
	355	360	365
10	AAT GTC CAC AGG ACA GAA GCC ATT GAG AGA GCA AGG TTG CAC ATA GGC Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly		1152
	370	375	380
15	AAA GGT GTG CAG TTG GAA TGT AAA GGT GAA GGT GAT GTT TGG GTC AGG Lys Gly Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg		1200
	385	390	395
	TGC CTT AGT GAC CAC GCG GTC TTT GTA CAG AGT TAC TAC TTA GAC AGA Cys Leu Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg		1248
	405	410	415
20	GAA GCT GGG CGT GCA CCT GGA GAT GCT GTT CAT AAG ATC TAC CCA AGT Glu Ala Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser		1296
	420	425	430
25	GCA TAT ATA AAG GTC TTT GAT TTG CGT CAG TGT CAT CGA CAG ATG CAG Ala Tyr Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln		1344
	435	440	445
30	CAG CAG GCG GCT ACT GCA CAA GCT GCA GCA GCT GCC CAG GCA GCA GCC Gln Gln Ala Ala Thr Ala Gln Ala Ala Ala Gln Ala Ala Ala		1392
	450	455	460
35	GTG GCA GGA AAC ATC CCT GGC CCA GGA TCA GTA GGT GGA ATA GCT CCA Val Ala Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro		1440
	465	470	475
	485	490	495
40	GCT ATC AGT CTG TCA GCT GCT GGA ATT GGT GTT GAT GAC CTT CGT Ala Ile Ser Leu Ser Ala Ala Gly Ile Gly Val Asp Asp Leu Arg		1488
	500	505	510
45	CGC TTA TGC ATA CTC AGG ATG AGT TTT GTG AAA GGC TGG GGA CCG GAT Arg Leu Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp		1536
	515	520	525
50	TAC CCA AGA CAG AGC ATC AAA GAA ACA CCT TGC TGG ATT GAA ATT CAC Tyr Pro Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His		1584
	530	535	540
55	TTA CAC CGG GCC CTC CAG CTC CTA GAC GAA GTA CTT CAT ACC ATG CCG Leu His Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro		1632
	545	550	555
	ATT GCA GAC CCA CAA CCT TTA GAC TGG GAT CCA CCG GTC GCC ACC ATG Ile Ala Asp Pro Gln Pro Leu Asp Trp Asp Pro Pro Val Ala Thr Met		1680
	560		
	GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC		1728

174

175

	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
	565	570	575
5	GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		1776
	580	585	590
10	GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		1824
	595	600	605
	ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		1872
	610	615	620
15	ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		1920
	625	630	635
20	CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		1968
	645	650	655
25	ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		2016
	660	665	670
30	AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		2064
	675	680	685
	GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		2112
	690	695	700
35	TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		2160
	705	710	715
40	ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		2208
	725	730	735
45	CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		2256
	740	745	750
50	GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		2304
	755	760	765
	AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		2352
	770	775	780
55	ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA		2397

175

176

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 785 790 795

5 (2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 amino acids
- (B) TYPE: amino acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

	Met	Asp	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys
	1					5			10						15	
20	Leu	Ser	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser
								20		25				30		
	Glu	Thr	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys
								35		40			45			
25	Glu	Lys	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn
								50		55			60			
	Gly	Ala	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly
								65		70		75		80		
	Arg	Leu	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala
								85		90			95			
30	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val
								100		105			110			
	Lys	Tyr	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val
								115		120			125			
35	Asn	Pro	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser
								130		135			140			
	Gly	Leu	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp
								145		150		155		160		
	Glu	Tyr	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly
								165		170			175			
40	His	Ser	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr
								180		185			190			
	Glu	Thr	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala
								195		200			205			
45	Thr	Ser	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln
								210		215			220			
	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile
								225		230		235		240		
	Ala	Ser	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln
								245		250			255			
50	Pro	Ala	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Trp	Thr	Gly	Ser	Arg	
								260		265			270			
	Thr	Ala	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu
								275		280			285			
55	Gln	His	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val
								290		295			300			
	His	Asn	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro

176

	305	310	315	320
	Glu Tyr Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly			
	325	330	335	
5	Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly			
	340	345	350	
	Tyr Val Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser			
	355	360	365	
	Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly			
	370	375	380	
10	Lys Gly Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg			
	385	390	395	400
	Cys Leu Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg			
	405	410	415	
	Glu Ala Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser			
15	420	425	430	
	Ala Tyr Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln			
	435	440	445	
	Gln Gln Ala Ala Thr Ala Gln Ala Ala Ala Ala Gln Ala Ala Ala			
	450	455	460	
20	Val Ala Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro			
	465	470	475	480
	Ala Ile Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg			
	485	490	495	
	Arg Leu Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp			
25	500	505	510	
	Tyr Pro Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His			
	515	520	525	
	Leu His Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro			
	530	535	540	
30	Ile Ala Asp Pro Gln Pro Leu Asp Trp Asp Pro Pro Val Ala Thr Met			
	545	550	555	560
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
	565	570	575	
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
35	580	585	590	
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
	595	600	605	
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
	610	615	620	
40	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
	625	630	635	640
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
	645	650	655	
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
45	660	665	670	
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
	675	680	685	
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
	690	695	700	
50	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
	705	710	715	720
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
	725	730	735	
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
55	740	745	750	
	Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			

178

	755	760	765
	Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
	770	775	780
	Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
5	785	790	795

(2) INFORMATION FOR SEQ ID NO:78:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 1...3135

20 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

25	ATG GCG GGC TGG ATC CAG GCC CAG CAG CTG CAG GGA GAC GCG CTG CGC Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln Gly Asp Ala Leu Arg 1 5 10 15	48
30	CAG ATG CAG GTG CTG TAC GGC CAG CAC TTC CCC ATC GAG GTC CGG CAC Gln Met Gln Val Leu Tyr Gln His Phe Pro Ile Glu Val Arg His 20 25 30	96
35	TAC TTG GCC CAG TGG ATT GAG AGC CAG CCA TGG GAT GCC ATT GAC TTG Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu 35 40 45	144
40	GAC AAT CCC CAG GAC AGA GCA GCC CAA ACC CAG CTC CTG GAG GGC CTG Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Glu Gly Leu 50 55 60	192
45	GTG CAG GAG CTG CAG AAG GCG GAG CAC CAG GTG GGG GAA GAT GGG Val Gln Glu Leu Gln Lys Ala Glu His Gln Val Gly Glu Asp Gly 65 70 75 80	240
50	TTT TTA CTG AAG ATC AAG CTG GGG CAC TAC GCC ACG CAG CTC CAG AAA Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys 85 90 95	288
55	ACA TAT GAC CGC TGC CCC CTG GAG CTG GTC CGC TGC ATC CGG CAC ATT Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile 100 105 110	336
	CTG TAC AAT GAA CAG AGG CTG GTC CGA GAA GCC AAC AAT TGC AGC TCT Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser 115 120 125	384
	CCG GCT GGG ATC CTG GTT GAC GCC ATG TCC CAG AAG CAC CTT CAG ATC 432	432

178

179

	Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile			
	130	135	140	
5	AAC CAG ACA TTT GAG GAG CTG CGA CTG GTC ACG CAG GAC ACA GAG AAT		480	
	Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn			
	145	150	155	160
10	GAG CTG AAG AAA CTG CAG CAG ACT CAG GAG TAC TTC ATC ATC CAG TAC		528	
	Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr			
	165	170	175	
15	CAG GAG AGC CTG AGG ATC CAA GCT CAG TTT GCC CAG CTG GCC CAG CTG		576	
	Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu			
	180	185	190	
20	AGC CCC CAG GAG CGT CTG AGC CGG GAG ACG GCC CTC CAG CAG AAG CAG		624	
	Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Gln Lys Gln			
	195	200	205	
25	GTG TCT CTG GAG GCC TGG TTG CAG CGT GAG GCA CAG ACA CTG CAG CAG		672	
	Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln			
	210	215	220	
30	TAC CGC GTG GAG CTG GCC GAG AAG CAC CAG AAG ACC CTG CAG CTG CTG		720	
	Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu			
	225	230	235	240
35	CGG AAG CAG CAG ACC ATC ATC CTG GAT GAC GAG CTG ATC CAG TGG AAG		768	
	Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys			
	245	250	255	
40	CGG CGG CAG CAG CTG GCC GGG AAC GGC GGG CCC CCC GAG GGC AGC CTG		816	
	Arg Arg Gln Gln Leu Ala Gly Asn Gly Pro Pro Glu Gly Ser Leu			
	260	265	270	
45	GAC GTG CTA CAG TCC TGG TGT GAG AAG TTG GCC GAG ATC ATC TGG CAG		864	
	Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln			
	275	280	285	
50	AAC CGG CAG CAG ATC CGC AGG GCT GAG CAC CTC TGC CAG CAG CTG CCC		912	
	Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu Cys Gln Gln Leu Pro			
	290	295	300	
55	ATC CCC GGC CCA GTG GAG GAG ATG CTG GCC GAG GTC AAC GCC ACC ATC		960	
	Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu Val Asn Ala Thr Ile			
	305	310	315	320
60	ACG GAC ATT ATC TCA GCC CTG GTG ACC AGC ACA TTC ATC ATT GAG AAG		1008	
	Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr Phe Ile Ile Glu Lys			
	325	330	335	
65	CAG CCT CCT CAG GTC CTG AAG ACC CAG ACC AAG TTT GCA GCC ACC GTA		1056	
	Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys Phe Ala Ala Thr Val			
	340	345	350	
70	CGC CTG CTG GTG GGC GGG AAG CTG AAC GTG CAC ATG AAT CCC CCC CAG		1104	

179

180

	Arg Leu Leu Val Gly Gly Lys Leu Asn Val His Met Asn Pro Pro Gln		
	355	360	365
5	GTG AAG GCC ACC ATC ATC AGT GAG CAG CAG GCC AAG TCT CTG CTT AAA Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala Lys Ser Leu Leu Lys		1152
	370	375	380
10	AAT GAG AAC ACC CGC AAC GAG TGC AGT GGT GAG ATC CTG AAC AAC TGC Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu Ile Leu Asn Asn Cys		1200
	385	390	395
	TGC GTG ATG GAG TAC CAC CAA GCC ACG GGC ACC CTC AGT GCC CAC TTC Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr Leu Ser Ala His Phe		1248
	405	410	415
15	AGG AAC ATG TCA CTG AAG AGG ATC AAG CGT GCT GAC CGG CGG GGT GCA Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala Asp Arg Arg Gly Ala		1296
	420	425	430
20	GAG TCC GTG ACA GAG GAG AAG TTC ACA GTC CTG TTT GAG TCT CAG TTC Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu Phe Glu Ser Gln Phe		1344
	435	440	445
25	AGT GTT GGC AGC AAT GAG CTT GTG TTC CAG GTG AAG ACT CTG TCC CTA Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val Lys Thr Leu Ser Leu		1392
	450	455	460
30	CCT GTG GTT GTC ATC GTC CAC GGC AGC CAG GAC CAC AAT GCC ACG GCT Pro Val Val Val Ile Val His Gly Ser Gln Asp His Asn Ala Thr Ala		1440
	465	470	475
	ACT GTG CTG TGG GAC AAT GCC TTT GCT GAG CCG GGC AGG GTG CCA TTT Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro Gly Arg Val Pro Phe		1488
	485	490	495
35	GCC GTG CCT GAC AAA GTG CTG TGG CCG CAG CTG TGT GAG GCG CTC AAC Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu Cys Glu Ala Leu Asn		1536
	500	505	510
40	ATG AAA TTC AAG GCC GAA GTG CAG AGC AAC CGG GGC CTG ACC AAG GAG Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg Gly Leu Thr Lys Glu		1584
	515	520	525
45	AAC CTC GTG TTC CTG GCG CAG AAA CTG TTC AAC AAC AGC AGC AGC CAC Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn Asn Ser Ser Ser His		1632
	530	535	540
50	CTG GAG GAC TAC AGT GGC CTG TCC GTG TCC TGG TCC CAG TTC AAC AGG Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp Ser Gln Phe Asn Arg		1680
	545	550	555
	GAG AAC TTG CCG GGC TGG AAC TAC ACC TTC TGG CAG TGG TTT GAC GGG Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp Gln Trp Phe Asp Gly		1728
	565	570	575
55	GTG ATG GAG GTG TTG AAG AAG CAC CAC AAG CCC CAC TGG AAT GAT GGG		1776

180

181

	Val Met Glu Val Leu Lys His His Lys Pro His Trp Asn Asp Gly		
	580	585	590
5	GCC ATC CTA GGT TTT GTG AAT AAG CAA CAG GCC CAC GAC CTG CTC ATC Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala His Asp Leu Leu Ile		1824
	595	600	605
10	AAC AAG CCC GAC GGG ACC TTC TTG CGC TTT AGT GAC TCA GAA ATC Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe Ser Asp Ser Glu Ile		1872
	610	615	620
15	GGG GGC ATC ACC ATC GCC TGG AAG TTT GAC TCC CCG GAA CGC AAC CTG Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser Pro Glu Arg Asn Leu		1920
	625	630	635
	640		
20	TGG AAC CTG AAA CCA TTC ACC ACG CGG GAT TTC TCC ATC AGG TCC CTG Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe Ser Ile Arg Ser Leu		1968
	645	650	655
25	GCT GAC CGG CTG GGG GAC CTG AGC TAT CTC ATC TAT GTG TTT CCT GAC Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile Tyr Val Phe Pro Asp		2016
	660	665	670
30	CGC CCC AAG GAT GAG GTC TTC TCC AAG TAC TAC ACT CCT GTG CTG GCT Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr Thr Pro Val Leu Ala		2064
	675	680	685
35	AAA GCT GTT GAT GGA TAT GTG AAA CCA CAG ATC AAG CAA GTG GTC CCT Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile Lys Gln Val Val Pro		2112
	690	695	700
40	GAG TTT GTG AAT GCA TCT GCA GAT GCT GGG GGC AGC AGC GCC ACG TAC Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly Ser Ser Ala Thr Tyr		2160
	705	710	715
	720		
45	705	710	715
50	ATG GAC CAG GCC CCC TCC CCA GCT GTG TGC CCC CAG GCT CCC TAT AAC Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro Gln Ala Pro Tyr Asn		2208
	725	730	735
55	ATG TAC CCA CAG AAC CCT GAC CAT GTA CTC GAT CAG GAT GGA GAA TTC Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp Gln Asp Gly Glu Phe		2256
	740	745	750
60	GAC CTG GAT GAG ACC ATG GAT GTG GCC AGG CAC GTG GAG GAA CTC TTA Asp Leu Asp Glu Thr Met Asp Val Ala Arg His Val Glu Glu Leu Leu		2304
	755	760	765
65	CGC CGA CCA ATG GAC AGT CTT GAC TCC CGC CTC TCG CCC CCT GCC GGT Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu Ser Pro Pro Ala Gly		2352
	770	775	780
70	CTT TTC ACC TCT GCC AGA GGC TCC CTC TCA TGG GTA CCG CGG GCC CGG Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser Trp Val Pro Arg Ala Arg		2400
	785	790	795
	800		
75	GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC		2448

182

	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr		
	805	810	815
5	GGG GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His		2496
	820	825	830
10	AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys		2544
	835	840	845
	CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp		2592
	850	855	860
15	CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg		2640
	865	870	875
20	TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro		2688
	885	890	895
25	GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn		2736
	900	905	910
30	TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn		2784
	915	920	925
	CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu		2832
	930	935	940
35	GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met		2880
	945	950	955
40	GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His		2928
	965	970	975
45	AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn		2976
	980	985	990
50	ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu		3024
	995	1000	1005
	AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His		3072
	1010	1015	1020
55	ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG		3120

182

183

1025	Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
	1030 1035 1040

5	GAC GAG CTG TAC AAG TAA Asp Glu Leu Tyr Lys 1045	3138
---	--	------

(2) INFORMATION FOR SEQ ID NO:79:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1045 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln Gly Asp Ala Leu Arg			
1	5	10	15
Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His			
20	25	30	
Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu			
35	40	45	
Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Glu Gly Leu			
50	55	60	
Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly			
65	70	75	80
Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys			
85	90	95	
Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile			
100	105	110	
Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser			
115	120	125	
Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile			
130	135	140	
Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn			
145	150	155	160
Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr			
165	170	175	
Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu			
180	185	190	
Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Gln Lys Gln			
195	200	205	
Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln			
210	215	220	
Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu			
225	230	235	240
Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys			
245	250	255	
Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro Pro Glu Gly Ser Leu			
260	265	270	
Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln			

183

184

	275	280	285
	Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu Cys Gln Gln Leu Pro		
	290	295	300
5	Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu Val Asn Ala Thr Ile		
	305	310	315
	Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr Phe Ile Ile Glu Lys		320
	325	330	335
10	Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys Phe Ala Ala Thr Val		
	340	345	350
	Arg Leu Leu Val Gly Gly Lys Leu Asn Val His Met Asn Pro Pro Gln		
	355	360	365
	Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala Lys Ser Leu Leu Lys		
	370	375	380
15	Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu Ile Leu Asn Asn Cys		
	385	390	395
	Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr Leu Ser Ala His Phe		400
	405	410	415
	Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala Asp Arg Arg Gly Ala		
	420	425	430
20	Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu Phe Glu Ser Gln Phe		
	435	440	445
	Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val Lys Thr Leu Ser Leu		
	450	455	460
25	Pro Val Val Val Ile Val His Gly Ser Gln Asp His Asn Ala Thr Ala		
	465	470	475
	Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro Gly Arg Val Pro Phe		480
	485	490	495
	Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu Cys Glu Ala Leu Asn		
	500	505	510
30	Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg Gly Leu Thr Lys Glu		
	515	520	525
	Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn Asn Ser Ser Ser His		
	530	535	540
35	Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp Ser Gln Phe Asn Arg		
	545	550	555
	Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp Gln Trp Phe Asp Gly		560
	565	570	575
	Val Met Glu Val Leu Lys Lys His His Lys Pro His Trp Asn Asp Gly		
	580	585	590
40	Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala His Asp Leu Ile		
	595	600	605
	Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe Ser Asp Ser Glu Ile		
	610	615	620
45	Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser Pro Glu Arg Asn Leu		
	625	630	635
	Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe Ser Ile Arg Ser Leu		640
	645	650	655
	Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile Tyr Val Phe Pro Asp		
	660	665	670
50	Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr Thr Pro Val Leu Ala		
	675	680	685
	Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile Lys Gln Val Val Pro		
	690	695	700
55	Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly Ser Ser Ala Thr Tyr		
	705	710	715
	Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro Gln Ala Pro Tyr Asn		720

185

	725	730	735
	Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp Gln Asp Gly Glu Phe		
	740	745	750
5	Asp Leu Asp Glu Thr Met Asp Val Ala Arg His Val Glu Glu Leu Leu		
	755	760	765
	Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu Ser Pro Pro Ala Gly		
	770	775	780
	Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser Trp Val Pro Arg Ala Arg		
	785	790	795
10	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr		
	805	810	815
	Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His		
	820	825	830
15	Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys		
	835	840	845
	Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp		
	850	855	860
	Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg		
	865	870	875
20	Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro		
	885	890	895
	Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn		
	900	905	910
25	Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn		
	915	920	925
	Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu		
	930	935	940
	Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met		
	945	950	955
30	Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His		
	965	970	975
	Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn		
	980	985	990
35	Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu		
	995	1000	1005
	Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His		
	1010	1015	1020
	Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met		
	1025	1030	1035
40	Asp Glu Leu Tyr Lys		
	1045		

(2) INFORMATION FOR SEQ ID NO:80:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TGGGATCCTC AGGCCGTGCT GCTGGCCG

28

55

(2) INFORMATION FOR SEQ ID NO:81:

185

186

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
GTTATCCCGG TGGCTTCCGC CTTTCCC

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGGATCCGA GAACTCTATA TCCCATC 27
25

(2) INFORMATION FOR SEQ ID NO:83:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGGGATCCTT AGAAGTCTAT ATCCCCATC 28

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
50 GTCTCGAGCC ATGAAACGCC CCGAGCGG

(2) INFORMATION FOR SEQ ID NO:85:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid

187

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGAATTCTC GTCTGATTTC TGGCAGGAGG

30

(2) INFORMATION FOR SEQ ID NO:86:

- 10 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

20 GTGAATTCTT TACGTCTGAT TTCTGGCAGG

30

(2) INFORMATION FOR SEQ ID NO:87:

- 25 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCTCGAGCC ATGGACGAAC TGTTCCCCCT CATC

34

35 (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATCCAA GGAGCTGATC TGACTCAGCA G

31

(2) INFORMATION FOR SEQ ID NO:89:

- 50 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

55

187

188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGATCCTT AGGAGCTGAT CTGACTCAGC AG

32

5 (2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

15

CCTCCTAACCG TTATCATGGA CCATTATGAT TC

32

(2) INFORMATION FOR SEQ ID NO:91:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

30

CCTCCTGGAT CCCTGCGCAG GATGATGGTC CAG

33

(2) INFORMATION FOR SEQ ID NO:92:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGATGGAAGC TTCAATGGCT GCCATCCGGA AGAAACTGGT GATTG

45

(2) INFORMATION FOR SEQ ID NO:93:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

55

GGATGGGGAT CCTCACAAAGA CAAGGCAACC AGATTTTTTC TTCCCC

45

188

189

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGGAAGCTTC CATGAGCGAG ACGGTCATC

29

(2) INFORMATION FOR SEQ ID NO:95:

15

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

25

CCCGGATCCT CAGGGAGAAC CCCGCTTC

28

(2) INFORMATION FOR SEQ ID NO:96:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTGAATTCGA CCATGGAGCG GCCCCCCGGGG

30

40

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

50

GTGGTACCCA TTCTGTTAAC CAACTCC

27

(2) INFORMATION FOR SEQ ID NO:98:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

189

190

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGGTACCTC ATTCTGTTAA CCAACTCC

28

10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

20

GTCTCGAGAG ATGCTGTCCC GTGGGTGG

28

(2) INFORMATION FOR SEQ ID NO:100:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

35

GTGAATTCCGC TTCCCTCTTGA GGGAAACC

27

(2) INFORMATION FOR SEQ ID NO:101:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTGAATTCAC TTCCCTCTTGA GGGAAACC

27

50

(2) INFORMATION FOR SEQ ID NO:102:

55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

190

191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTCTCGAGCC ATGGAGAACT TCCAAAAGG

29

5

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGGATCCCA GAGTCGAAGA TGGGGTAC

28

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

30

GTGGATCCTC AGAGTCGAAG ATGGGGTAC

29

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGAATTCTGG CGATGCCAGA CCCCCGCGGCG

30

45

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTGGATCCCA GGCACAGGCA GCCTCAGCCT TC

32

191

192

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTGGATCCTC AGGCACAGGC AGCCTCAGCC TTC

33

15

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 2616 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 1...2613

- (D) OTHER INFORMATION:

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATG GTG AGC AAG GGC GAG GAG	CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu	Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5	10 15	

35

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25	30

40

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40	45

45

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55	60

50

CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70	75 80

55

CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90	95

CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
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192

193

	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100	105	110
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		384
	115	120	125
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		432
	130	135	140
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		480
	145	150	155
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		528
	165	170	175
20	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		576
	180	185	190
25	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		624
	195	200	205
30	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		672
	210	215	220
35	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		720
	225	230	235
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Met Pro Asp Pro		768
	245	250	255
40	GCG GCG CAC CTG CCC TTC TAC GGC AGC ATC TCG CGT GCC GAG GCC Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala		816
	260	265	270
45	GAG GAG CAC CTG AAG CTG GCG GGC ATG GCG GAC GGG CTC TTC CTG CTG Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu		864
	275	280	285
50	CGC CAG TGC CTG CGC TCG CTG GGC TAT GTG CTG TCG CTC GTG CAC Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His		912
	290	295	300
55	GAT GTG CGC TTC CAC CAC TTT CCC ATC GAG CGC CAG CTC AAC GGC ACC Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr		960
	305	310	315
	TAC GCC ATT GCC GGC GGC AAA GCG CAC TGT GGA CCG GCA GAG CTC TGC		1008

194

	Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys		
	325	330	335
5	GAG TTC TAC TCG CGC GAC CCC GAC GGG CTG CCC TGC AAC CTG CGC AAG Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys		1056
	340	345	350
10	CCG TGC AAC CGG CCG TCG GGC CTC GAG CCG CAG CCG GGG GTC TTC GAC Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp		1104
	355	360	365
15	TGC CTG CGA GAC GCC ATG GTG CGT GAC TAC GTG CGC CAG ACG TGG AAG Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys		1152
	370	375	380
20	CTG GAG GGC GAG GCC CTG GAG CAG GCC ATC ATC AGC CAG GCC CCG CAG Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser Gln Ala Pro Gln		1200
	385	390	395
	395	400	
25	Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr		1248
	405	410	415
30	CAC AGC AGC CTG ACG CGT GAG GAG GCC GAG CGC AAA CTT TAC TCT GGG His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys Leu Tyr Ser Gly		1296
	420	425	430
	425	430	
35	GCG CAG ACC GAC GGC AAG TTC CTG CTG AGG CCG CGG AAG GAG CAG GGC Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys Glu Gln Gly		1344
	435	440	445
	440	445	
40	ACA TAC GCC CTG TCC CTC ATC TAT GGG AAG ACG GTG TAC CAC TAC CTC Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu		1392
	450	455	460
	455	460	
45	460		
50	ATC AGC CAA GAC AAG GCG GGC AAG TAC TGC ATT CCC GAG GGC ACC AAG Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu Gly Thr Lys		1440
	465	470	475
	470	475	480
	475	480	
55	480		
50	TTT GAC ACG CTC TGG CAG CTG GTG GAG TAT CTG AAG CTG AAG GCG GAC Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp		1488
	485	490	495
	490	495	
55	495		
45	GGG CTC ATC TAC TGC CTG AAG GAG GCC TGC CCC AAC AGC AGT GCC AGC Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser		1536
	500	505	510
	505	510	
50	AAC GCC TCA GGG GCT GCT CCC ACA CTC CCA GCC CAC CCA TCC ACG Asn Ala Ser Gly Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr		1584
	515	520	525
	520	525	
55	525		
50	TTG ACT CAT CCT CAG AGA CGA ATC GAC ACC CTC AAC TCA GAT GGA TAC Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr		1632
	530	535	540
	535	540	
55	540		
50	ACC CCT GAG CCA GCA CGC ATA ACG TCC CCA GAC AAA CCG CGG CCG ATG		1680
	550		

195

	Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met			
545	550	555	560	
5	CCC ATG GAC ACG AGC GTG TAT GAG AGC CCC TAC AGC GAC CCA GAG GAG Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu	565	570	575
10	CTC AAG GAC AAG AAG CTC TTC CTG AAG CGC GAT AAC CTC CTC ATA GCT Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala	580	585	590
15	GAC ATT GAA CTT GGC TGC GGC AAC TTT GGC TCA GTG CGC CAG GGC GTG Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val	595	600	605
20	TAC CGC ATG CGC AAG AAG CAG ATC GAC GTG GCC ATC AAG GTG CTG AAG Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys	610	615	620
25	CAG GGC ACG GAG AAG GCA GAC ACG GAA GAG ATG ATG CGC GAG GCG CAG Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln	625	630	635
30	ATC ATG CAC CAG CTG GAC AAC CCC TAC ATC GTG CCG CTC ATT GGC GTC Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val	645	650	655
35	TGC CAG GCC GAG GCC CTC ATG CTG GTC ATG GAG ATG GCT GGG GGC GGG Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly	660	665	670
40	CCG CTG CAC AAG TTC CTG GTC GGC AAG AGG GAG GAG ATC CCT GTG AGC Pro Leu His Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser	675	680	685
45	AAT GTG GCC GAG CTG CTG CAC CAG GTG TCC ATG GGG ATG AAG TAC CTG Asn Val Ala Glu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu	690	695	700
50	GAG GAG AAG AAC TTT GTG CAC CGT GAC CTG GCG GCC CGC AAC GTC CTG Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu	705	710	715
55	CTG GTT AAC CGG CAC TAC GCC AAG ATC AGC GAC TTT GGC CTC TCC AAA Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys	725	730	735
55	GCA CTG GGT GCC GAC GAC TAC TAC ACT GCC CGC TCA GCA GGG AAG Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys	740	745	750
55	TGG CCG CTC AAG TGG TAC GCA CCC GAA TGC ATC AAC TTC CGC AAG TTC Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe	755	760	765
55	TCC AGC CGC AGC GAT GTC TGG AGC TAT GGG GTC ACC ATG TGG GAG GCC			2352

195

196

	Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala	
	770 775 780	
5	TTG TCC TAC GGC CAG AAG CCC TAC AAG AAG ATG AAA GGG CCG GAG GTC Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val 785 790 795 800	2400
10	ATG GCC TTC ATC GAG CAG GGC AAG CGG ATG GAG TGC CCA CCA GAG TGT Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys 805 810 815	2448
15	CCA CCC GAA CTG TAC GCA CTC ATG AGT GAC TGC TGG ATC TAC AAG TGG Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp 820 825 830	2496
20	GAG GAT CGC CCC GAC TTC CTG ACC GTG GAG CAG CGC ATG CGA GCC TGT Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys 835 840 845	2544
25	TAC TAC AGC CTG GCC AGC AAG GTG GAA GGG CCC CCA GGC AGC ACA CAG Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln 850 855 860	2592
	AAG GCT GAG GCT GCC TGT GCC TGA	2616
	Lys Ala Glu Ala Ala Cys Ala 865 870	

(2) INFORMATION FOR SEQ ID NO:109:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 871 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
	1 5 10 15
45	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
	20 25 30
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
	35 40 45
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50	50 55 60
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
	65 70 75 80
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
	85 90 95
55	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
	100 105 110
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

197

	115	120	125
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
	130	135	140
5	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
	145	150	155
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		160
	165	170	175
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
	180	185	190
10	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
	195	200	205
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
	210	215	220
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
15	225	230	235
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Met Pro Asp Pro		240
	245	250	255
	Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala		
	260	265	270
20	Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu		
	275	280	285
	Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His		
	290	295	300
25	Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr		
	305	310	315
	Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys		320
	325	330	335
	Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys		
	340	345	350
30	Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp		
	355	360	365
	Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys		
	370	375	380
	Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser Gln Ala Pro Gln		
35	385	390	395
	Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr		400
	405	410	415
	His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys Leu Tyr Ser Gly		
	420	425	430
40	Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys Glu Gln Gly		
	435	440	445
	Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu		
	450	455	460
45	Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu Gly Thr Lys		
	465	470	475
	Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp		480
	485	490	495
	Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser		
	500	505	510
50	Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr		
	515	520	525
	Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr		
	530	535	540
	Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met		
55	545	550	555
	Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu		560

198

	565	570	575
	Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala		
	580	585	590
5	Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Val Arg Gln Gly Val		
	595	600	605
	Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys		
	610	615	620
	Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln		
	625	630	635
10	Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val		
	645	650	655
	Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly		
	660	665	670
15	Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser		
	675	680	685
	Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu		
	690	695	700
	Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu		
	705	710	715
20	Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys		
	725	730	735
	Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys		
	740	745	750
25	Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe		
	755	760	765
	Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala		
	770	775	780
	Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val		
	785	790	795
30	Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys		
	805	810	815
	Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp		
	820	825	830
35	Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys		
	835	840	845
	Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln		
	850	855	860
	Lys Ala Glu Ala Ala Cys Ala		
40	865	870	

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 1...2595

- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

199

	ATG CCA GAC CCC GCG GCG CAC CTG CCC TTC TTC TAC GGC AGC ATC TCG Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser 1 5 10 15	48
5	CGT GCC GAG GCC GAG GAG CAC CTG AAG CTG GCG GGC ATG GCG GAC GGG Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly 20 25 30	96
10	CTC TTC CTG CTG CGC CAG TGC CTG CGC TCG CTG GGC GGC TAT GTG CTG Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu 35 40 45	144
15	TCG CTC GTG CAC GAT GTG CGC TTC CAC CAC TTT CCC ATC GAG CGC CAG Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln 50 55 60	192
20	CTC AAC GGC ACC TAC GCC ATT GCC GGC GGC AAA GCG CAC TGT GGA CCG Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro 65 70 75 80	240
25	GCA GAG CTC TGC GAG TTC TAC TCG CGC GAC CCC GAC GGG CTG CCC TGC Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys 85 90 95	288
30	AAC CTG CGC AAG CCG TGC AAC CGG CCG TCG GGC CTC GAG CCG CAG CCG Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro 100 105 110	336
35	GGG GTC TTC GAC TGC CTG CGA GAC GCC ATG GTG CGT GAC TAC GTG CGC Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg 115 120 125	384
40	CAG ACG TGG AAG CTG GAG GGC GAG GCC CTG GAG CAG GCC ATC ATC AGC Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser 130 135 140	432
45	CAG GCC CCG CAG GTG GAG AAG CTC ATT GCT ACG ACG GCC CAC GAG CGG Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg 145 150 155 160	480
50	ATG CCC TGG TAC CAC AGC AGC CTG ACG CGT GAG GAG GCC GAG CGC AAA Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys 165 170 175	528
55	CTT TAC TCT GGG GCG CAG ACC GAC GGC AAG TTC CTG CTG AGG CCG CGG Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg 180 185 190	576
60	AAG GAG CAG GGC ACA TAC GCC CTG TCC CTC ATC TAT GGG AAG ACG GTG Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val 195 200 205	624
65	TAC CAC TAC CTC ATC AGC CAA GAC AAG GCG GGC AAG TAC TGC ATT CCC Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro 210 215 220	672

200

	GAG GGC ACC AAG TTT GAC ACG CTC TGG CAG CTG GTG GAG TAT CTG AAG Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys 225 230 235 240	720
5	CTG AAG GCG GAC GGG CTC ATC TAC TGC CTG AAG GAG GCC TGC CCC AAC Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn 245 250 255	768
10	AGC AGT GCC AGC AAC GCC TCA GGG GCT GCT CCC ACA CTC CCA GCC Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala 260 265 270	816
15	CAC CCA TCC ACG TTG ACT CAT CCT CAG AGA CGA ATC GAC ACC CTC AAC His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn 275 280 285	864
20	TCA GAT GGA TAC ACC CCT GAG CCA GCA CGC ATA ACG TCC CCA GAC AAA Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys 290 295 300	912
25	CCG CGG CCG ATG CCC ATG GAC ACG AGC GTG TAT GAG AGC CCC TAC AGC Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser 305 310 315 320	960
30	GAC CCA GAG GAG CTC AAG GAC AAG AAG CTC TTC CTG AAG CGC GAT AAC Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn 325 330 335	1008
35	CTC CTC ATA GCT GAC ATT GAA CTT GGC TGC GGC AAC TTT GGC TCA GTG Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val 340 345 350	1056
40	CGC CAG GGC GTG TAC CGC ATG CGC AAG AAG CAG ATC GAC GTG GCC ATC Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile 355 360 365	1104
45	AAG GTG CTG AAG CAG GGC ACG GAG AAG GCA GAC ACG GAA GAG ATG ATG Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met 370 375 380	1152
50	CGC GAG GCG CAG ATC ATG CAC CAG CTG GAC AAC CCC TAC ATC GTG CGG Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg 385 390 395 400	1200
55	CTC ATT GGC GTC TGC CAG GCC GAG GCC CTC ATG CTG GTC ATG GAG ATG Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met 405 410 415	1248
	GCT GGG GGC GGG CCG CTG CAC AAG TTC CTG GTC GGC AAG AGG GAG GAG Ala Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu 420 425 430	1296
	ATC CCT GTG AGC AAT GTG GCC GAG CTG CTG CAC CAG GTG TCC ATG GGG Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly 435 440 445	1344

	ATG AAG TAC CTG GAG GAG AAG AAC TTT GTG CAC CGT GAC CTG GCG GCC Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala 450 455 460	1392
5	CGC AAC GTC CTG CTG GTT AAC CGG CAC TAC GCC AAG ATC AGC GAC TTT Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe 465 470 475 480	1440
10	GGC CTC TCC AAA GCA CTG GGT GCC GAC GAC AGC TAC TAC ACT GCC CGC Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg 485 490 495	1488
15	TCA GCA GGG AAG TGG CCG CTC AAG TGG TAC GCA CCC GAA TGC ATC AAC Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn 500 505 510	1536
20	TTC CGC AAG TTC TCC AGC CGC AGC GAT GTC TGG AGC TAT GGG GTC ACC Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr 515 520 525	1584
	ATG TGG GAG GCC TTG TCC TAC GGC CAG AAG CCC TAC AAG AAG ATG AAA Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys 530 535 540	1632
25	GGG CCG GAG GTC ATG GCC TTC ATC GAG CAG GGC AAG CGG ATG GAG TGC Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys 545 550 555 560	1680
30	CCA CCA GAG TGT CCA CCC GAA CTG TAC GCA CTC ATG AGT GAC TGC TGG Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp 565 570 575	1728
35	ATC TAC AAG TGG GAG GAT CGC CCC GAC TTC CTG ACC GTG GAG CAG CGC Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg 580 585 590	1776
40	ATG CGA GCC TGT TAC TAC AGC CTG GCC AGC AAG GTG GAA GGG CCC CCA Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro 595 600 605	1824
	GGC AGC ACA CAG AAG GCT GAG GCT GCC TGT GGC TGG GAT CCA CCG GTC Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala Trp Asp Pro Pro Val 610 615 620	1872
45	GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 625 630 635 640	1920
50	ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 645 650 655	1968
55	TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 660 665 670	2016

202

	TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val 675 680 685	2064
5	ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His 690 695 700	2112
10	ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 705 710 715 720	2160
15	CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 725 730 735	2208
20	GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 740 745 750	2256
25	AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 755 760 765	2304
30	GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 770 775 780	2352
35	AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 785 790 795 800	2400
40	GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 805 810 815	2448
45	GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser 820 825 830	2496
50	GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 835 840 845	2544
55	GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 850 855 860	2592
	AAG TAA Lys 865	2598

55 (2) INFORMATION FOR SEQ ID NO:111:

202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

	Met	Pro	Asp	Pro	Ala	Ala	His	Leu	Pro	Phe	Phe	Tyr	Gly	Ser	Ile	Ser	
1					5					10					15		
15	Arg	Ala	Glu	Ala	Glu	Glu	His	Leu	Lys	Leu	Ala	Gly	Met	Ala	Asp	Gly	
					20					25					30		
	Leu	Phe	Leu	Leu	Arg	Gln	Cys	Leu	Arg	Ser	Leu	Gly	Gly	Tyr	Val	Leu	
					35					40					45		
	Ser	Leu	Val	His	Asp	Val	Arg	Phe	His	His	Phe	Pro	Ile	Glu	Arg	Gln	
20					50					55					60		
	Leu	Asn	Gly	Thr	Tyr	Ala	Ile	Ala	Gly	Gly	Lys	Ala	His	Cys	Gly	Pro	
		65				70					75					80	
	Ala	Glu	Leu	Cys	Glu	Phe	Tyr	Ser	Arg	Asp	Pro	Asp	Gly	Leu	Pro	Cys	
					85					90					95		
25	Asn	Leu	Arg	Lys	Pro	Cys	Asn	Arg	Pro	Ser	Gly	Leu	Glu	Pro	Gln	Pro	
					100					105					110		
	Gly	Val	Phe	Asp	Cys	Leu	Arg	Asp	Ala	Met	Val	Arg	Asp	Tyr	Val	Arg	
					115					120					125		
	Gln	Thr	Trp	Lys	Leu	Glu	Gly	Glu	Ala	Leu	Glu	Gln	Ala	Ile	Ile	Ser	
					130					135					140		
30	Gln	Ala	Pro	Gln	Val	Glu	Lys	Leu	Ile	Ala	Thr	Thr	Ala	His	Glu	Arg	
					145					150					155		
	Met	Pro	Trp	Tyr	His	Ser	Ser	Leu	Thr	Arg	Glu	Glu	Ala	Glu	Arg	Lys	
						165					170					175	
35	Leu	Tyr	Ser	Gly	Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	Arg	Pro	Arg	
						180					185					190	
	Lys	Glu	Gln	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	Lys	Thr	Val	
						195					200					205	
	Tyr	His	Tyr	Leu	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro	
40					210					215					220		
	Glu	Gly	Thr	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys	
					225					230					235		
		Leu	Lys	Ala	Asp	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	
						245					250					255	
45	Ser	Ser	Ala	Ser	Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala	
						260					265					270	
	His	Pro	Ser	Thr	Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn	
						275					280					285	
	Ser	Asp	Gly	Tyr	Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys	
50						290					295					300	
	Pro	Arg	Pro	Met	Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser	
							305					310			315		
	Asp	Pro	Glu	Glu	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Lys	Arg	Asp	Asn	
							325					330				335	
55	Leu	Leu	Ile	Ala	Asp	Ile	Glu	Leu	Gly	Cys	Gly	Asn	Phe	Gly	Ser	Val	
							340					345				350	
	Arg	Gln	Gly	Val	Tyr	Arg	Met	Arg	Lys	Lys	Gln	Ile	Asp	Val	Ala	Ile	

204

	355	360	365
	Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met		
	370	375	380
5	Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg		
	385	390	395
	Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met		
	405	410	415
	Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu		
	420	425	430
10	Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly		
	435	440	445
	Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala		
	450	455	460
15	Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe		
	465	470	475
	Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Ala Arg		
	485	490	495
	Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn		
	500	505	510
20	Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr		
	515	520	525
	Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys		
	530	535	540
25	Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys		
	545	550	555
	Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp		
	565	570	575
	Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg		
	580	585	590
30	Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro		
	595	600	605
	Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala Trp Asp Pro Pro Val		
	610	615	620
	Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
35	625	630	635
	Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val		
	645	650	655
	Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
	660	665	670
40	Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
	675	680	685
	Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His		
	690	695	700
45	Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
	705	710	715
	Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg		
	725	730	735
	Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu		
	740	745	750
50	Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu		
	755	760	765
	Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln		
	770	775	780
55	Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
	785	790	795
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		800

205

	805	810	815
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
	820	825	830
5	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu		
	835	840	845
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr		
	850	855	860
	Lys		
	865		

10

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1632

(D) OTHER INFORMATION:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATG GAG AAC TTC CAA AAG GTG GAA AAG ATC GGA GAG GGC ACG TAC GGA	48
Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly	
30 1 5 10 15	
GTG GTG TAC AAA GCC AGA AAC AAG TTG ACG GGA GAG GTG GTG GCG CTT	96
Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu	
20 25 30	
AAG AAA ATC CGC CTG GAC ACT GAG ACT GAG GGT GTG CCC AGT ACT GCC	144
Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala	
35 40 45	
ATC CGA GAG ATC TCT CTG CTT AAG GAG CTT AAC CAT CCT AAT ATT GTC	192
Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val	
50 55 60	
AAG CTG CTG GAT GTC ATT CAC ACA GAA AAT AAA CTC TAC CTG GTT TTT	240
Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe	
45 65 70 75 80	
GAA TTT CTG CAC CAA GAT CTC AAG AAA TTC ATG GAT GCC TCT GCT CTC	288
Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu	
50 85 90 95	
ACT GGC ATT CCT CTT CCC CTC ATC AAG AGC TAT CTG TTC CAG CTG CTC	336
Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu	
100 105 110	
CAG GGC CTA GCT TTC TGC CAT TCT CAT CGG GTC CTC CAC CGA GAC CTT	384

205

206

	Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu		
	115	120	125
5	AAA CCT CAG AAT CTG CTT ATT AAC ACA GAG GGG GCC ATC AAG CTA GCA Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala		432
	130	135	140
10	GAC TTT GGA CTA GCC AGA GCT TTT GGA GTC CCT GTT CGT ACT TAC ACC Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr		480
	145	150	155
15	CAT GAG GTG GTG ACC CTG TGG TAC CGA GCT CCT GAA ATC CTC CTG GGC His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly		528
	165	170	175
20	TCG AAA TAT TAT TCC ACA GCT GTG GAC ATC TGG AGC CTG GGC TGC ATC Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile Trp Ser Leu Gly Cys Ile		576
	180	185	190
25	TTT GCT GAG ATG GTG ACT CGC CGG GCC CTG TTC CCT GGA GAT TCT GAG Phe Ala Glu Met Val Thr Arg Arg Ala Leu Phe Pro Gly Asp Ser Glu		624
	195	200	205
30	ATT GAC CAG CTC TTC CGG ATC TTT CGG ACT CTG GGG ACC CCA GAT GAG Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr Leu Gly Thr Pro Asp Glu		672
	210	215	220
35	GTG GTG TGG CCA GGA GTT ACT TCT ATG CCT GAT TAC AAG CCA AGT TTC Val Val Trp Pro Gly Val Thr Ser Met Pro Asp Tyr Lys Pro Ser Phe		720
	225	230	235
40	240		
45	CCC AAG TGG GCC CGG CAA GAT TTT AGT AAA GTT GTA CCT CCC CTG GAT Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys Val Val Pro Pro Leu Asp		768
	245	250	255
50	GAA GAT GGA CGG AGC TTG TTA TCG CAA ATG CTG CAC TAC GAC CCT AAC Glu Asp Gly Arg Ser Leu Leu Ser Gln Met Leu His Tyr Asp Pro Asn		816
	260	265	270
55	AAG CGG ATT TCG GCC AAG GCA GCC CTG GCT CAC CCT TTC TTC CAG GAT Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala His Pro Phe Phe Gln Asp		864
	275	280	285
60	GTG ACC AAG CCA GTA CCC CAT CTT CGA CTC TGG GAT CCA CCG GTC GCC Val Thr Lys Pro Val Pro His Leu Arg Leu Trp Asp Pro Pro Val Ala		912
	290	295	300
65	ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile		960
	305	310	315
70	Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser		1008
	325	330	335
75	CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC		1056.
	335		

207

	Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe		
	340	345	350
5	ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr		1104
	355	360	365
10	ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met		1152
	370	375	380
15	AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln		1200
	385	390	395
	400	405	410
20	GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala		1248
	415	420	425
	430	435	440
25	GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys		1296
	445	450	455
	460	465	470
30	TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		1344
	475	480	485
35	AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly		1392
	490	495	500
	505	510	515
40	AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp		1440
	520	525	530
45	CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu		1488
	535	540	545
50	TTC GTG ACC GCC GCG GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG T Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		1536
	550	555	560
	565	570	575
	580	585	590
	595	600	605
	610	615	620
	625	630	635
	640	645	650
	655	660	665
	670	675	680
	685	690	695
	700	705	710
	715	720	725
	730	735	740
	745	750	755
	760	765	770
	775	780	785
	790	795	800
	805	810	815
	820	825	830
	835	840	845
	850	855	860
	865	870	875
	880	885	890
	895	900	905
	910	915	920
	925	930	935
	940	945	950
	955	960	965
	970	975	980
	985	990	995
	1000	1005	1010
	1015	1020	1025
	1030	1035	1040
	1045	1050	1055
	1060	1065	1070
	1075	1080	1085
	1090	1095	1100
	1105	1110	1115
	1120	1125	1130
	1135	1140	1145
	1150	1155	1160
	1165	1170	1175
	1180	1185	1190
	1195	1200	1205
	1210	1215	1220
	1225	1230	1235
	1240	1245	1250
	1255	1260	1265
	1270	1275	1280
	1285	1290	1295
	1300	1305	1310
	1315	1320	1325
	1330	1335	1340
	1345	1350	1355
	1360	1365	1370
	1375	1380	1385
	1390	1395	1400
	1405	1410	1415
	1420	1425	1430
	1435	1440	1445
	1450	1455	1460
	1465	1470	1475
	1480	1485	1490
	1495	1500	1505
	1510	1515	1520
	1525	1530	1535
	1540	1545	1550
	1555	1560	1565
	1570	1575	1580
	1585	1590	1595
	1600	1605	1610
	1615	1620	1625
	1630	1635	1640
	1645	1650	1655
	1660	1665	1670
	1675	1680	1685
	1690	1695	1700
	1705	1710	1715
	1720	1725	1730
	1735	1740	1745
	1750	1755	1760
	1765	1770	1775
	1780	1785	1790
	1795	1800	1805
	1810	1815	1820
	1825	1830	1835
	1840	1845	1850
	1855	1860	1865
	1870	1875	1880
	1885	1890	1895
	1900	1905	1910
	1915	1920	1925
	1930	1935	1940
	1945	1950	1955
	1960	1965	1970
	1975	1980	1985
	1990	1995	2000
	2005	2010	2015
	2020	2025	2030
	2035	2040	2045
	2050	2055	2060
	2065	2070	2075
	2080	2085	2090
	2095	2100	2105
	2110	2115	2120
	2125	2130	2135
	2140	2145	2150
	2155	2160	2165
	2170	2175	2180
	2185	2190	2195
	2200	2205	2210
	2215	2220	2225
	2230	2235	2240
	2245	2250	2255
	2260	2265	2270
	2275	2280	2285
	2290	2295	2300
	2305	2310	2315
	2320	2325	2330
	2335	2340	2345
	2350	2355	2360
	2365	2370	2375
	2380	2385	2390
	2395	2400	2405
	2410	2415	2420
	2425	2430	2435
	2440	2445	2450
	2455	2460	2465
	2470	2475	2480
	2485	2490	2495
	2500	2505	2510
	2515	2520	2525
	2530	2535	2540
	2545	2550	2555
	2560	2565	2570
	2575	2580	2585
	2590	2595	2600
	2605	2610	2615
	2620	2625	2630
	2635	2640	2645
	2650	2655	2660
	2665	2670	2675
	2680	2685	2690
	2695	2700	2705
	2710	2715	2720
	2725	2730	2735
	2740	2745	2750
	2755	2760	2765
	2770	2775	2780
	2785	2790	2795
	2800	2805	2810
	2815	2820	2825
	2830	2835	2840
	2845	2850	2855
	2860	2865	2870
	2875	2880	2885
	2890	2895	2900
	2905	2910	2915
	2920	2925	2930
	2935	2940	2945
	2950	2955	2960
	2965	2970	2975
	2980	2985	2990
	2995	3000	3005
	3010	3015	3020
	3025	3030	3035
	3040	3045	3050
	3055	3060	3065
	3070	3075	3080
	3085	3090	3095
	3100	3105	3110
	3115	3120	3125
	3130	3135	3140
	3145	3150	3155
	3160	3165	3170
	3175	3180	3185
	3190	3195	3200
	3205	3210	3215
	3220	3225	3230
	3235	3240	3245
	3250	3255	3260
	3265	3270	3275
	3280	3285	3290
	3295	3300	3305
	3310	3315	3320
	3325	3330	3335
	3340	3345	3350
	3355	3360	3365
	3370	3375	3380
	3385	3390	3395
	3400	3405	3410
	3415	3420	3425
	3430	3435	3440
	3445	3450	3455
	3460	3465	3470
	3475	3480	3485
	3490	3495	3500
	3505	3510	3515
	3520	3525	3530
	3535	3540	3545
	3550	3555	3560
	3565	3570	3575
	3580	3585	3590
	3595	3600	3605
	3610	3615	3620
	3625	3630	3635
	3640	3645	3650
	3655	3660	3665
	3670	3675	3680
	3685	3690	3695
	3700	3705	3710
	3715	3720	3725
	3730	3735	3740
	3745	3750	3755
	3760	3765	3770
	3775	3780	3785
	3790	3795	3800
	3805	3810	3815
	3820	3825	3830
	3835	3840	3845
	3850	3855	3860
	3865	3870	3875
	3880	3885	3890
	3895	3900	3905
	3910	3915	3920
	3925	3930	3935
	3940	3945	3950
	3955	3960	3965
	3970	3975	3980
	3985	3990	3995
	4000	4005	4010
	4015	4020	4025
	4030	4035	4040
	4045	4050	4055
	4060	4065	4070
	4075	4080	4085
	4090	4095	4100
	4105	4110	4115
	4120	4125	4130
	4135	4140	4145
	4150	4155	4160
	4165	4170	4175
	4180	4185	4190
	4195	4200	4205
	4210	4215	4220
	4225	4230	4235
	4240	4245	4250
	4255	4260	4265
	4270	4275	4280
	4285	4290	4295
	4300	4305	4310
	4315	4320	4325
	4330	4335	4340
	4345	4350	4355
	4360	4365	4370
	4375	4380	4385
	4390	4395	4400
	4405	4410	4415
	4420	4425	4430
	4435	4440	4445
	4450	4455	4460
	4465	4470	4475
	4480	4485	4490
	4495	4500	4505
	4510	4515	4520
	4525	4530	4535
	4540	4545	4550
	4555	4560	4565
	4570	4575	4580
	4585	4590	4595
	4600	4605	4610
	4615	4620	4625
	4630	4635	4640
	4645	4650	4655
	4660	4665	4670
	4675	4680	4685
	4690	4695	4700
	4705	4710	4715
	4720	4725	4730
	4735	4740	

208

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

	Met	Glu	Asn	Phe	Gln	Lys	Val	Glu	Lys	Ile	Gly	Glu	Gly	Thr	Tyr	Gly
1							5				10					15
	Val	Val	Tyr	Lys	Ala	Arg	Asn	Lys	Leu	Thr	Gly	Glu	Val	Val	Ala	Leu
									20		25					30
15	Lys	Lys	Ile	Arg	Leu	Asp	Thr	Glu	Thr	Glu	Gly	Val	Pro	Ser	Thr	Ala
							35			40					45	
	Ile	Arg	Glu	Ile	Ser	Leu	Leu	Lys	Glu	Leu	Asn	His	Pro	Asn	Ile	Val
							50			55					60	
20	Lys	Leu	Leu	Asp	Val	Ile	His	Thr	Glu	Asn	Lys	Leu	Tyr	Leu	Val	Phe
							65			70			75		80	
	Glu	Phe	Leu	His	Gln	Asp	Leu	Lys	Phe	Met	Asp	Ala	Ser	Ala	Leu	
							85			90					95	
	Thr	Gly	Ile	Pro	Leu	Pro	Ile	Lys	Ser	Tyr	Leu	Phe	Gln	Leu	Leu	
							100			105					110	
25	Gln	Gly	Leu	Ala	Phe	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	Asp	Leu
							115			120					125	
	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Thr	Glu	Gly	Ala	Ile	Lys	Leu	Ala
							130			135					140	
	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Val	Arg	Thr	Tyr	Thr
30							145			150			155		160	
	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Gly	
							165			170			175			
	Ser	Lys	Tyr	Tyr	Ser	Thr	Ala	Val	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Ile
							180			185			190			
35	Phe	Ala	Glu	Met	Val	Thr	Arg	Arg	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu
							195			200			205			
	Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Thr	Leu	Gly	Thr	Pro	Asp	Glu
							210			215			220			
	Val	Val	Trp	Pro	Gly	Val	Thr	Ser	Met	Pro	Asp	Tyr	Lys	Pro	Ser	Phe
40							225			230			235		240	
	Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys	Val	Val	Pro	Pro	Leu	Asp
							245			250			255			
	Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met	Leu	His	Tyr	Asp	Pro	Asn
							260			265			270			
45	Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala	His	Pro	Phe	Phe	Gln	Asp
							275			280			285			
	Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu	Trp	Asp	Pro	Pro	Val	Ala
							290			295			300			
	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile
50							305			310			315		320	
	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser
							325			330			335			
	Gly	Glu	Gly	Gly	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe
							340			345			350			
55	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr
							355			360			365			

208

209

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 370 375 380
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 385 390 395 400
 5 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 405 410 415
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 420 425 430
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 10 435 440 445
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 450 455 460
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 465 470 475 480
 15 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 485 490 495
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 500 505 510
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 20 515 520 525
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 530 535 540

(2) INFORMATION FOR SEQ ID NO:114:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1635 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 35 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1632
 (D) OTHER INFORMATION:
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
45 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
50 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
55 TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

209

	210		
	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80		240
5	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95		288
10	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110		336
15	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125		384
20	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140		432
	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160		480
25	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175		528
30	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190		576
35	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205		624
40	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220		672
	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240		720
45	GGA CTC AGA TCT CGA GCC ATG GAG AAC TTC CAA AAG GTG GAA AAG ATC Gly Leu Arg Ser Arg Ala Met Glu Asn Phe Gln Lys Val Glu Lys Ile 245 250 255		768
50	GGA GAG GGC ACG TAC GGA GTT GTG TAC AAA GCC AGA AAC AAG TTG ACG Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala Arg Asn Lys Leu Thr 260 265 270		816
55	GGA GAG GTG GTG GCG CTT AAG AAA ATC CGC CTG GAC ACT GAG ACT GAG Gly Glu Val Val Ala Leu Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu 275 280 285		864

	211	
	GGT GTG CCC AGT ACT GCC ATC CGA GAG ATC TCT CTG CTT AAG GAG CTT Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu 290 295 300	912
5	AAC CAT CCT AAT ATT GTC AAG CTG CTG GAT GTC ATT CAC ACA GAA AAT Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn 305 310 315 320	960
10	AAA CTC TAC CTG TTT GAA TTT CTG CAC CAA GAT CTC AAG AAA TTC Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe 325 330 335	1008
15	ATG GAT GCC TCT GCT CTC ACT GGC ATT CCT CTT CCC CTC ATC AAG AGC Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser 340 345 350	1056
20	TAT CTG TTC CAG CTG CTC CAG GGC CTA GCT TTC TGC CAT TCT CAT CGG Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg 355 360 365	1104
25	GTC CTC CAC CGA GAC CTT AAA CCT CAG AAT CTG CTT ATT AAC ACA GAG Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu 370 375 380	1152
30	GGG GCC ATC AAG CTA GCA GAC TTT GGA CTA GCC AGA GCT TTT GGA GTC Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val 385 390 395 400	1200
35	CCT GTT CGT ACT TAC ACC CAT GAG GTG GTG ACC CTG TGG TAC CGA GCT Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala 405 410 415	1248
40	CCT GAA ATC CTC CTG GGC TCG AAA TAT TAT TCC ACA GCT GTG GAC ATC Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile 420 425 430	1296
45	TGG AGC CTG GGC TGC ATC TTT GCT GAG ATG GTG ACT CGC CGG GCC CTG Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu 435 440 445	1344
50	TTC CCT GGA GAT TCT GAG ATT GAC CAG CTC TTC CGG ATC TTT CGG ACT Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr 450 455 460	1392
55	CTG GGG ACC CCA GAT GAG GTG GTG TGG CCA GGA GTT ACT TCT ATG CCT Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro 465 470 475 480	1440
	GAT TAC AAG CCA AGT TTC CCC AAG TGG GCC CGG CAA GAT TTT AGT AAA Asp Tyr Lys Pro Ser Phe Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys 485 490 495	1488
	GTT GTA CCT CCC CTG GAT GAA GAT GGA CGG AGC TTG TTA TCG CAA ATG Val Val Pro Pro Leu Asp Glu Asp Gly Arg Ser Leu Leu Ser Gln Met 500 505 510	1536

212

CTG CAC TAC GAC CCT AAC AAG CGG ATT TCG GCC AAG GCA GCC CTG GCT	1584
Leu His Tyr Asp Pro Asn Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala	
515	520
525	
5 CAC CCT TTC TTC CAG GAT GTG ACC AAG CCA GTA CCC CAT CTT CGA CTC T	1633
His Pro Phe Phe Gln Asp Val Thr Lys Pro Val Pro His Leu Arg Leu	
530	535
540	

GA	1635
10	

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
25 1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
30 20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
40 50	55	60	
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
45 65	70	75	80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
50 85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
55 100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
60 115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
65 130	135	140	
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
70 145	150	155	160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
75 165	170	175	
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
80 180	185	190	
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
85 195	200	205	
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
90 210	215	220	
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
95 225	230	235	240
Gly Leu Arg Ser Arg Ala Met Glu Asn Phe Gln Lys Val Glu Lys Ile			
100 245	250	255	
Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala Arg Asn Lys Leu Thr			

212

213

	260	265	270
	Gly Glu Val Val Ala Leu Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu		
	275	280	285
5	Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu		
	290	295	300
	Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn		
	305	310	315
	Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe		
	325	330	335
10	Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser		
	340	345	350
	Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg		
	355	360	365
15	Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu		
	370	375	380
	Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val		
	385	390	395
	Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala		
	405	410	415
20	Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile		
	420	425	430
	Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu		
	435	440	445
	Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr		
25	450	455	460
	Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro		
	465	470	475
	Asp Tyr Lys Pro Ser Phe Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys		
	485	490	495
30	Val Val Pro Pro Leu Asp Glu Asp Gly Arg Ser Leu Leu Ser Gln Met		
	500	505	510
	Leu His Tyr Asp Pro Asn Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala		
	515	520	525
35	His Pro Phe Phe Gln Asp Val Thr Lys Pro Val Pro His Leu Arg Leu		
	530	535	540

(2) INFORMATION FOR SEQ ID NO:116:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...2529

50 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG
55 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

48

213

214

	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
5	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
10	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
15	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
20	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
25	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
30	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
35	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAC AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480
	145 150 155 160	
40	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	528
	165 170 175	
45	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	576
	180 185 190	
	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	624
	195 200 205	
50	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	672
	210 215 220	
55	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	720
	225 230 235 240	

214

215

	GGA CTC AGA TCT CGA GAG ATG CTG TCC CGT GGG TGG TTT CAC CGA GAC Gly Leu Arg Ser Arg Glu Met Leu Ser Arg Gly Trp Phe His Arg Asp 245 250 255	768
5	CTC AGT GGG CTG GAT GCA GAG ACC CTG CTC AAG GGC CGA GGT GTC CAC Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys Gly Arg Gly Val His 260 265 270	816
10	GGT AGC TTC CTG GCT CGG CCC AGT CGC AAG AAC CAG GGT GAC TTC TCG Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser 275 280 285	864
15	CTC TCC GTC AGG GTG GGG GAT CAG GTG ACC CAT ATT CGG ATC CAG AAC Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile Gln Asn 290 295 300	912
20	TCA GGG GAT TTC TAT GAC CTG TAT GGA GGG GAG AAG TTT GCG ACT CTG Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Glu Lys Phe Ala Thr Leu 305 310 315 320	960
25	ACA GAG CTG GTG GAG TAC ACT CAG CAG CAG GGT GTC CTG CAG GAC Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp 325 330 335	1008
30	CGC GAC GGC ACC ATC ATC CAC CTC AAG TAC CCG CTG AAC TGC TCC GAT Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys Ser Asp 340 345 350	1056
35	CCC ACT AGT GAG AGG TGG TAC CAT GGC CAC ATG TCT GGC GGG CAG GCA Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly Gln Ala 355 360 365	1104
40	GAG ACG CTG CTG CAG GCC AAG GGC GAG CCC TGG ACG TTT CTT GTG CGT Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg 370 375 380	1152
45	GAG AGC CTC AGC CAG CCT GGA GAC TTC GTG CTT TCT GTG CTC AGT GAC Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp 385 390 395 400	1200
50	CAG CCC AAG GCT GGC CCA GGC TCC CCG CTC AGG GTC ACC CAC ATC AAG Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys 405 410 415	1248
55	GTC ATG TGC GAG GGT GGA CGC TAC ACA GTG GGT TTG GAG ACC TTC Val Met Cys Glu Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe 420 425 430	1296
55	GAC AGC CTC ACG GAC CTG GTA GAG CAT TTC AAG AAG ACG GGG ATT GAG Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu 435 440 445	1344
55	GAG GCC TCA GGC GCC TTT GTC TAC CTG CGG CAG CCG TAC TAT GCC ACG Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr 450 455 460	1392

216

	AGG GTG AAT GCG GCT GAC ATT GAG AAC CGA GTG TTG GAA CTG AAC AAG Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val Leu Glu Leu Asn Lys 465 470 475 480	1440
5	AAG CAG GAG TCC GAG GAT ACA GCC AAG GCT GGC TTC TGG GAG GAG TTT Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe 485 490 495	1488
10	GAG AGT TTG CAG AAG CAG GAG GTG AAG AAC TTG CAC CAG CGT CTG GAA Glu Ser Leu Gln Lys Glu Val Lys Asn Leu His Gln Arg Leu Glu 500 505 510	1536
15	GGG CAG CGG CCA GAG AAC AAG GGC AAG AAC CGC TAC AAG AAC ATT CTC Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu 515 520 525	1584
20	CCC TTT GAC CAC ACC CGA GTG ATC CTG CAG GGA CGG GAC AGT AAC ATC Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly Arg Asp Ser Asn Ile 530 535 540	1632
25	CCC GGG TCC GAC TAC ATC AAT GCC AAC TAC ATC AAG AAC CAG CTG CTA Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu 545 550 555 560	1680
30	GGC CCT GAT GAG AAC GCT AAG ACC TAC ATC GCC AGC CAG GGC TGT CTG Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu 565 570 575	1728
35	GAG GCC ACG GTC AAT GAC TTC TGG CAG ATG GCG TGG CAG GAG AAC AGC Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu Asn Ser 580 585 590	1776
40	CGT GTC ATC GTC ATG ACC ACC CGA GAG GTG GAG AAA GGC CGG AAC AAA Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg Asn Lys 595 600 605	1824
45	TGC GTC CCA TAC TGG CCC GAG GTG GGC ATG CAG CGT GCT TAT GGG CCC Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln Arg Ala Tyr Gly Pro 610 615 620	1872
50	TAC TCT GTG ACC AAC TGC GGG GAG CAT GAC ACA ACC GAA TAC AAA CTC Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr Lys Leu 625 630 635 640	1920
55	CGT ACC TTA CAG GTC TCC CCG CTG GAC AAT GGA GAC CTG ATT CGG GAG Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu 645 650 655	1968
60	ATC TGG CAT TAC CAG TAC CTG AGC TGG CCC GAC CAT GGG GTC CCC AGT Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His Gly Val Pro Ser 660 665 670	2016
65	GAG CCT GGG GGT GTC CTC AGC TTC CTG GAC CAG ATC AAC CAG CGG CAG Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln 675 680 685	2064

217

	GAA AGT CTG CCT CAC GCA GGG CCC ATC ATC GTG CAC TGC AGC GCC GGC Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser Ala Gly 690 695 700	2112
5	ATC GGC CGC ACA GGC ACC ATC ATT GTC ATC GAC ATG CTC ATG GAG AAC Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met Glu Asn 705 710 715 720	2160
10	ATC TCC ACC AAG GGC CTG GAC TGT GAC ATT GAC ATC CAG AAG ACC ATC Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile 725 730 735	2208
15	CAG ATG GTG CGG GCG CAG CGC TCG GGC ATG GTG CAG ACG GAG GCG CAG Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln 740 745 750	2256
20	TAC AAG TTC ATC TAC GTG GCC ATC GCC CAG TTC ATT GAA ACC ACT AAG Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys 755 760 765	2304
	AAG AAG CTG GAG GTC CTG CAG TCG CAG AAG GGC CAG GAG TCG GAG TAC Lys Lys Leu Glu Val Leu Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr 770 775 780	2352
25	GGG AAC ATC ACC TAT CCC CCA GCC ATG AAG AAT GCC CAT GCC AAG GCC Gly Asn Ile Thr Tyr Pro Pro Ala Met Lys Asn Ala His Ala Lys Ala 785 790 795 800	2400
30	TCC CGC ACC TCG TCC AAA CAC AAG GAG GAT GTG TAT GAG AAC CTG CAC Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val Tyr Glu Asn Leu His 805 810 815	2448
35	ACT AAG AAC AAG AGG GAG GAG AAA GTG AAG AAG CAG CGG TCA GCA GAC Thr Lys Asn Lys Arg Glu Glu Lys Val Lys Lys Gln Arg Ser Ala Asp 820 825 830	2496
40	AAG GAG AAG AGC AAG GGT TCC CTC AAG AGG AAG TGA Lys Glu Lys Ser Lys Gly Ser Leu Lys Arg Lys 835 840	2532

(2) INFORMATION FOR SEQ ID NO:117:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

218

	1	5	10	15
	Val	Glu	Leu	Asp
	Gly	Gly	Gly	Asp
	Asp	Asp	Val	Asn
	Val	Asn	Gly	His
			Lys	Phe
			Ser	Ser
			Val	Gly
		20	25	30
	Glu	Gly	Gly	Asp
	Asp	Ala	Thr	Tyr
	Ala	Thr	Tyr	Gly
			Lys	Leu
			Thr	Leu
			Lys	Phe
			Ile	
5		35	40	45
	Cys	Thr	Thr	Gly
	Thr	Gly	Lys	Leu
	Pro	Pro	Val	Trp
			Pro	Thr
			Leu	Val
			Thr	Thr
		50	55	60
	Leu	Thr	Tyr	Gly
	Thr	Gly	Val	Gln
	Gly	Cys	Phe	Ser
	Asp	Phe	Arg	Tyr
	Pro	Asp	Pro	Asp
			His	Met
			Lys	Lys
10	Gln	His	Asp	Phe
	Phe	Phe	Lys	Ser
			Ala	Met
			Met	Pro
			Glu	Gly
			Tyr	Val
			Gln	Glu
		85	90	95
	Arg	Thr	Ile	Phe
	Phe	Phe	Lys	Asp
			Asp	Asp
			Gly	Asn
			Tyr	Tyr
			Lys	Thr
			Arg	Ala
		100	105	110
	Val	Lys	Phe	Gly
	Asp	Thr	Leu	Val
			Asn	Arg
			Ile	Glu
			Leu	Lys
			Gly	
15		115	120	125
	Ile	Asp	Phe	Lys
	Phe	Lys	Glu	Asp
			Gly	Asn
			Ile	Leu
			Gly	His
			Lys	Lys
		130	135	140
	Asn	Tyr	Asn	Ser
	Ser	His	Asn	Val
			Tyr	Ile
			Met	Ala
			Asp	Lys
			Gln	Lys
		145	150	155
20	Gly	Ile	Lys	Val
	Asn	Phe	Lys	Ile
			Arg	His
			Asn	Ile
			Glu	Asp
			Gly	Ser
		165	170	175
	Val	Gln	Leu	Ala
	Ala	Asp	His	Tyr
			Gln	Gln
			Asn	Thr
			Pro	Ile
			Gly	Asp
		180	185	190
25	Pro	Val	Leu	Leu
	Pro	Asp	Asn	His
			Tyr	Leu
			Ser	Thr
			Gln	Ser
			Ala	Leu
		195	200	205
	Ser	Lys	Asp	Pro
	Pro	Asn	Glu	Lys
			Arg	Asp
			His	Met
			Val	Leu
			Leu	Glu
		210	215	220
	Val	Thr	Ala	Ala
	Gly	Ile	Thr	Leu
	Met	Asp	Glu	Leu
			Tyr	Tyr
			Lys	Ser
		225	230	235
30	Gly	Leu	Arg	Ser
	Arg	Glu	Met	Leu
			Ser	Arg
			Gly	Trp
			Phe	His
		245	250	255
	Leu	Ser	Gly	Leu
	Asp	Ala	Glu	Thr
			Leu	Leu
			Lys	Gly
		260	265	270
35	Gly	Ser	Phe	Leu
	Leu	Ala	Arg	Pro
			Ser	Arg
			Lys	Asn
		275	280	285
	Leu	Ser	Val	Arg
			Gly	Asp
			Gln	Va
		290	295	300
	Ser	Gly	Asp	Phe
			Tyr	Asp
			Leu	Tyr
			Gly	Gly
		305	310	315
40	Thr	Glu	Leu	Val
	Glu	Tyr	Tyr	Thr
			Gln	Gln
			Gln	Gly
		325	330	335
	Arg	Asp	Gly	Thr
			Ile	Ile
			His	Lys
			Leu	Lys
		340	345	350
45	Pro	Thr	Ser	Glu
	Arg	Trp	Tyr	His
			Gly	His
			Met	Ser
			Gly	Gly
		355	360	365
	Glu	Thr	Leu	Leu
	Gln	Ala	Lys	Gly
			Glu	Pro
			Trp	Thr
		370	375	380
	Glu	Ser	Leu	Ser
	Gln	Pro	Gly	Asp
			Phe	Val
			Leu	Ser
		385	390	395
50	Gln	Pro	Lys	Ala
			Gly	Pro
			Gly	Ser
			Pro	Leu
		405	410	415
	Val	Met	Cys	Glu
	Gly	Gly	Gly	Arg
			Tyr	Thr
			Val	Gly
		420	425	430
	Asp	Ser	Leu	Thr
			Asp	Leu
			Val	Glu
		435	440	445
55	Glu	Ala	Ser	Gly
			Ala	Phe
			Val	Tyr
			Leu	Arg
			Gln	Pro
			Tyr	Tyr
			Ala	Thr

219

	450	455	460
	Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val	Glu Leu Asn Lys	
	465	470	475
	Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala	Gly Phe Trp Glu Glu Phe	
5	485	490	495
	Glu Ser Leu Gln Lys Gln Glu Val Lys Asn	Leu His Gln Arg Leu Glu	
	500	505	510
	Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn	Arg Tyr Lys Asn Ile Leu	
	515	520	525
10	Pro Phe Asp His Ser Arg Val Ile Leu Gln	Gly Arg Asp Ser Asn Ile	
	530	535	540
	Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile	Lys Asn Gln Leu Leu	
	545	550	555
	Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala	Ser Gln Gly Cys Leu	
15	565	570	575
	Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala	Trp Gln Glu Asn Ser	
	580	585	590
	Arg Val Ile Val Met Thr Thr Arg Glu Val	Glu Lys Gly Arg Asn Lys	
	595	600	605
20	Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln	Arg Ala Tyr Gly Pro	
	610	615	620
	Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr	Thr Glu Tyr Lys Leu	
	625	630	635
	Arg Thr Leu Gln Val Ser Pro Leu Asp Asn	Gly Asp Leu Ile Arg Glu	
25	645	650	655
	Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His	Gly Val Pro Ser	
	660	665	670
	Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln	Ile Asn Gln Arg Gln	
	675	680	685
30	Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val	His Cys Ser Ala Gly	
	690	695	700
	Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp	Met Leu Met Glu Asn	
	705	710	715
	Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp	Ile Gln Lys Thr Ile	
35	725	730	735
	Gln Met Val Arg Ala Gln Arg Ser Gly Met Val	Gln Thr Glu Ala Gln	
	740	745	750
	Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln	Phe Ile Glu Thr Thr Lys	
	755	760	765
40	Lys Lys Leu Glu Val Leu Gln Ser Gln Lys	Gly Gln Glu Ser Glu Tyr	
	770	775	780
	Gly Asn Ile Thr Tyr Pro Pro Ala Met Lys Asn	Ala His Ala Lys Ala	
	785	790	795
	Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val	Tyr Glu Asn Leu His	
45	805	810	815
	Thr Lys Asn Lys Arg Glu Glu Lys Val Lys	Lys Gln Arg Ser Ala Asp	
	820	825	830
	Lys Glu Lys Ser Lys Gly Ser Leu Lys Arg Lys		
50	835	840	

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2562 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

220

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

5

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2559
 (D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATG CTG TCC CGT GGG TGG TTT CAC CGA GAC CTC AGT GGG CTG GAT GCA	48
Met Leu Ser Arg Gly Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala	
1 5 10 15	
GAG ACC CTG CTC AAG GGC CGA GGT GTC CAC GGT AGC TTC CTG GCT CGG	96
Glu Thr Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg	
20 25 30	
CCC AGT CGC AAG AAC CAG GGT GAC TTC TCG CTC TCC GTC AGG GTG GGG	144
Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly	
35 40 45	
GAT CAG GTG ACC CAT ATT CGG ATC CAG AAC TCA GGG GAT TTC TAT GAC	192
Asp Gln Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp	
50 55 60	
CTG TAT GGA GGG GAG AAG TTT GCG ACT CTG ACA GAG CTG GTG GAG TAC	240
Leu Tyr Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr	
65 70 75 80	
TAC ACT CAG CAG CAG GGT GTC CTG CAG GAC CGC GAC GGC ACC ATC ATC	288
Tyr Thr Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile	
85 90 95	
CAC CTC AAG TAC CCG CTG AAC TGC TCC GAT CCC ACT AGT GAG AGG TGG	336
His Leu Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp	
100 105 110	
TAC CAT GGC CAC ATG TCT GGC GGG CAG GCA GAG ACG CTG CTG CAG GCC	384
Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala	
115 120 125	
AAG GGC GAG CCC TGG ACG TTT CTT GTG CGT GAG AGC CTC AGC CAG CCT	432
Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro	
130 135 140	
GGA GAC TTC GTG CTT TCT GTG CTC AGT GAC CAG CCC AAG GCT GGC CCA	480
Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro	
145 150 155 160	
GGC TCC CCG CTC AGG GTC ACC CAC ATC AAG GTC ATG TGC GAG GGT GGA	528
Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly	
165 170 175	
CGC TAC ACA GTG GGT GGT TTG GAG ACC TTC GAC AGC CTC ACG GAC CTG	576

220

221

	Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu		
	180	185	190
5	GTA GAG CAT TTC AAG AAG ACG GGG ATT GAG GAG GCC TCA GGC GCC TTT Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe		624
	195	200	205
10	GTC TAC CTG CGG CAG CCG TAC TAT GCC ACG AGG GTG AAT GCG GCT GAC Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp		672
	210	215	220
15	ATT GAG AAC CGA GTG TTG GAA CTG AAC AAG AAG CAG GAG TCC GAG GAT Ile Glu Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp		720
	225	230	235
	240	245	250
20	ACA GCC AAG GCT GGC TTC TGG GAG GAG TTT GAG AGT TTG CAG AAG CAG Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln		768
	255	260	265
	270	275	280
25	AAG GGC AAG AAC CGC TAC AAG AAC ATT CTC CCC TTT GAC CAC AGC CGA Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg		864
	285	290	295
30	GTG ATC CTG CAG GGA CGG GAC AGT AAC ATC CCC GGG TCC GAC TAC ATC Val Ile Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile		912
	300	305	310
35	AAT GCC AAC TAC ATC AAG AAC CAG CTG CTA GGC CCT GAT GAG AAC GCT Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala		960
	320	325	330
	335	340	345
40	AAG ACC TAC ATC GCC AGC CAG GGC TGT CTG GAG GCC ACG GTC AAT GAC Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp		1008
	355	360	365
45	TTC TGG CAG ATG GCG TGG CAG GAG AAC AGC CGT GTC ATC GTC ATG ACC Phe Trp Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr		1056
	380	385	390
	395	400	405
50	ACC CGA GAG GTG GAG AAA GGC CGG AAC AAA TGC GTC CCA TAC TGG CCC Thr Arg Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro		1104
	410	415	420
55	GAG GTG GGC ATG CAG CGT GCT TAT GGG CCC TAC TCT GTG ACC AAC TGC Glu Val Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys		1152
	425	430	435
	440	445	450
	455	460	465
	470	475	480
	485	490	495
	500	505	510
	515	520	525
	530	535	540
	545	550	555
	560	565	570
	575	580	585
	590	595	600
	605	610	615
	620	625	630
	635	640	645
	650	655	660
	665	670	675
	680	685	690
	695	700	705
	710	715	720
	725	730	735
	740	745	750
	755	760	765
	770	775	780
	785	790	795
	800	805	810
	815	820	825
	830	835	840
	845	850	855
	860	865	870
	875	880	885
	890	895	900
	905	910	915
	920	925	930
	935	940	945
	950	955	960
	965	970	975
	980	985	990
	995	1000	1005
	1010	1015	1020
	1025	1030	1035
	1040	1045	1050
	1055	1060	1065
	1070	1075	1080
	1085	1090	1095
	1100	1105	1110
	1115	1120	1125
	1130	1135	1140
	1145	1150	1155
	1160	1165	1170
	1175	1180	1185
	1190	1195	1200
	1205	1210	1215
	1220	1225	1230
	1235	1240	1245
	1250	1255	1260
	1265	1270	1275
	1280	1285	1290
	1295	1300	1305
	1310	1315	1320
	1325	1330	1335
	1340	1345	1350
	1355	1360	1365
	1370	1375	1380
	1385	1390	1395
	1400	1405	1410
	1415	1420	1425
	1430	1435	1440
	1445	1450	1455
	1460	1465	1470
	1475	1480	1485
	1490	1495	1500
	1505	1510	1515
	1520	1525	1530
	1535	1540	1545
	1550	1555	1560
	1565	1570	1575
	1580	1585	1590
	1595	1600	1605
	1610	1615	1620
	1625	1630	1635
	1640	1645	1650
	1655	1660	1665
	1670	1675	1680
	1685	1690	1695
	1700	1705	1710
	1715	1720	1725
	1730	1735	1740
	1745	1750	1755
	1760	1765	1770
	1775	1780	1785
	1790	1795	1800
	1805	1810	1815
	1820	1825	1830
	1835	1840	1845
	1850	1855	1860
	1865	1870	1875
	1880	1885	1890
	1895	1900	1905
	1910	1915	1920
	1925	1930	1935
	1940	1945	1950
	1955	1960	1965
	1970	1975	1980
	1985	1990	1995
	2000	2005	2010
	2015	2020	2025
	2030	2035	2040
	2045	2050	2055
	2060	2065	2070
	2075	2080	2085
	2090	2095	2100
	2105	2110	2115
	2120	2125	2130
	2135	2140	2145
	2150	2155	2160
	2165	2170	2175
	2180	2185	2190
	2195	2200	2205
	2210	2215	2220
	2225	2230	2235
	2240	2245	2250
	2255	2260	2265
	2270	2275	2280
	2285	2290	2295
	2300	2305	2310
	2315	2320	2325
	2330	2335	2340
	2345	2350	2355
	2360	2365	2370
	2375	2380	2385
	2390	2395	2400
	2405	2410	2415
	2420	2425	2430
	2435	2440	2445
	2450	2455	2460
	2465	2470	2475
	2480	2485	2490
	2495	2500	2505
	2510	2515	2520
	2525	2530	2535
	2540	2545	2550
	2555	2560	2565
	2570	2575	2580
	2585	2590	2595
	2600	2605	2610
	2615	2620	2625
	2630	2635	2640
	2645	2650	2655
	2660	2665	2670
	2675	2680	2685
	2690	2695	2700
	2705	2710	2715
	2720	2725	2730
	2735	2740	2745
	2750	2755	2760
	2765	2770	2775
	2780	2785	2790
	2795	2800	2805
	2810	2815	2820
	2825	2830	2835
	2840	2845	2850
	2855	2860	2865
	2870	2875	2880
	2885	2890	2895
	2900	2905	2910
	2915	2920	2925
	2930	2935	2940
	2945	2950	2955
	2960	2965	2970
	2975	2980	2985
	2990	2995	3000
	3005	3010	3015
	3020	3025	3030
	3035	3040	3045
	3050	3055	3060
	3065	3070	3075
	3080	3085	3090
	3095	3100	3105
	3110	3115	3120
	3125	3130	3135
	3140	3145	3150
	3155	3160	3165
	3170	3175	3180
	3185	3190	3195
	3200	3205	3210
	3215	3220	3225
	3230	3235	3240
	3245	3250	3255
	3260	3265	3270
	3275	3280	3285
	3290	3295	3300
	3305	3310	3315
	3320	3325	3330
	3335	3340	3345
	3350	3355	3360
	3365	3370	3375
	3380	3385	3390
	3395	3400	3405
	3410	3415	3420
	3425	3430	3435
	3440	3445	3450
	3455	3460	3465
	3470	3475	3480
	3485	3490	3495
	3500	3505	3510
	3515	3520	3525
	3530	3535	3540
	3545	3550	3555
	3560	3565	3570
	3575	3580	3585
	3590	3595	3600
	3605	3610	3615
	3620	3625	3630
	3635	3640	3645
	3650	3655	3660
	3665	3670	3675
	3680	3685	3690
	3695	3700	3705
	3710	3715	3720
	3725	3730	3735
	3740	3745	3750
	3755	3760	3765
	3770	3775	3780
	3785	3790	3795
	3800	3805	3810
	3815	3820	3825
	3830	3835	3840
	3845	3850	3855
	3860	3865	3870
	3875	3880	3885
	3890	3895	3900
	3905	3910	3915
	3920	3925	3930
	3935	3940	3945
	3950	3955	3960
	3965	3970	3975
	3980	3985	3990
	3995	4000	4005
	4010	4015	4020
	4025	4030	4035
	4040	4045	4050
	4055	4060	4065
	4070	4075	4080
	4085	4090	4095
	4100	4105	4110
	4115	4120	4125
	4130	4135	4140
	4145	4150	4155
	4160	4165	4170
	4175	4180	4185
	4190	4195	4200
	4205	4210	4215
	4220	4225	4230
	4235	4240	4245
	4250	4255	4260
	4265	4270	4275
	4280	4285	4290
	4295	4300	4305
	4310	4315	4320
	4325	4330	4335
	4340	4345	4350
	4355	4360	4365
	4370	4375	4380
	4385	4390	4395
	4400	4405	4410
	4415	4420	4425
	4430	4435	4440
	4445	4450	4455
	4460	4465	4470
	4475	4480	4485
	4490	4495	4500
	4505	4510	4515
	4520	4525	4530
	4535	4540	4545
	4550	4555	4560
	4565	4570	4575

222

	Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr		
	405	410	415
5	CTG AGC TGG CCC GAC CAT GGG GTC CCC AGT GAG CCT GGG GGT GTC CTC Leu Ser Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu		1296
	420	425	430
10	AGC TTC CTG GAC CAG ATC AAC CAG CGG CAG GAA AGT CTG CCT CAC GCA Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala		1344
	435	440	445
	GGG CCC ATC ATC GTG CAC TGC AGC GCC GGC ATC GGC CGC ACA GGC ACC Gly Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr		1392
	450	455	460
15	ATC ATT GTC ATC GAC ATG CTC ATG GAG AAC ATC TCC ACC AAG GGC CTG Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu		1440
	465	470	475
20	480	485	490
	GAC TGT GAC ATT GAC ATC CAG AAG ACC ATC CAG ATG GTG CGG GCG CAG Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln		1488
	495	500	505
25	CGC TCG GGC ATG GTG CAG ACG GAG GCG CAG TAC AAG TTC ATC TAC GTG Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val		1536
	510	515	520
30	525	530	535
	GCC ATC GCC CAG TTC ATT GAA ACC ACT AAG AAG AAG CTG GAG GTC CTG Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu		1584
	540	545	550
35	555	560	565
	CAG TCG CAG AAG GGC CAG GAG TCG GAG TAC GGG AAC ATC ACC TAT CCC Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro		1632
	570	575	580
40	585	590	595
	CCA GCC ATG AAG AAT GCC CAT GCC AAG GCC TCC CGC ACC TCG TCC AAA Pro Ala Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys		1680
	595	600	605
45	610	615	620
	GAC AAG GAG GAT GTG TAT GAG AAC CTG CAC ACT AAG AAC AAG AGG GAG His Lys Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu		1728
	620	625	630
50	635	640	645
	650	655	660
55	665	670	675
	680	685	690
	695	700	705
	710	715	720
	725	730	735
	740	745	750
	755	760	765
	770	775	780
	785	790	795
	800	805	810
	815	820	825
	830	835	840
	845	850	855
	860	865	870
	875	880	885
	890	895	900
	905	910	915
	920	925	930
	935	940	945
	950	955	960
	965	970	975
	980	985	990
	995	1000	1005

222

223

	Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His		
625	630	635	640
5	AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys		1968
	645	650	655
10	CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp		2016
	660	665	670
	CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg		2064
	675	680	685
15	TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro		2112
	690	695	700
20	GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn		2160
	705	710	715
25	TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn		2208
	725	730	735
30	CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu		2256
	740	745	750
	GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met		2304
35	755	760	765
	GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His		2352
	770	775	780
40	AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn		2400
	785	790	795
45	800		
	ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu		2448
	805	810	815
	AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His		2496
50	820	825	830
	835	840	845
55	ATG GTC CTG CTG GAG TTC GTG ACC GCC GGG ATC ACT CTC GGC ATG Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met		2544
	845		
	GAC GAG CTG TAC AAG TAA		2562

Asp Glu Leu Tyr Lys
850

5 (2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 amino acids
- (B) TYPE: amino acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

	Met	Leu	Ser	Arg	Gly	Trp	Phe	His	Arg	Asp	Leu	Ser	Gly	Leu	Asp	Ala
	1			5				10			15					
20	Glu	Thr	Leu	Leu	Lys	Gly	Arg	Gly	Val	His	Gly	Ser	Phe	Leu	Ala	Arg
				20				25			30					
	Pro	Ser	Arg	Lys	Asn	Gln	Gly	Asp	Phe	Ser	Leu	Ser	Val	Arg	Val	Gly
				35				40			45					
25	Asp	Gln	Val	Thr	His	Ile	Arg	Ile	Gln	Asn	Ser	Gly	Asp	Phe	Tyr	Asp
				50				55			60					
	Leu	Tyr	Gly	Gly	Glu	Lys	Phe	Ala	Thr	Leu	Thr	Glu	Leu	Val	Glu	Tyr
				65				70			75			80		
	Tyr	Thr	Gln	Gln	Gly	Val	Leu	Gln	Asp	Arg	Asp	Gly	Thr	Ile	Ile	
				85				90			95					
30	His	Leu	Lys	Tyr	Pro	Leu	Asn	Cys	Ser	Asp	Pro	Thr	Ser	Glu	Arg	Trp
				100				105			110					
	Tyr	His	Gly	His	Met	Ser	Gly	Gly	Gln	Ala	Glu	Thr	Leu	Leu	Gln	Ala
				115				120			125					
35	Lys	Gly	Glu	Pro	Trp	Thr	Phe	Leu	Val	Arg	Glu	Ser	Leu	Ser	Gln	Pro
				130				135			140					
	Gly	Asp	Phe	Val	Leu	Ser	Val	Leu	Ser	Asp	Gln	Pro	Lys	Ala	Gly	Pro
				145				150			155			160		
	Gly	Ser	Pro	Leu	Arg	Val	Thr	His	Ile	Lys	Val	Met	Cys	Glu	Gly	Gly
				165				170			175					
40	Arg	Tyr	Thr	Val	Gly	Gly	Leu	Glu	Thr	Phe	Asp	Ser	Leu	Thr	Asp	Leu
				180				185			190					
	Val	Glu	His	Phe	Lys	Lys	Thr	Gly	Ile	Glu	Glu	Ala	Ser	Gly	Ala	Phe
				195				200			205					
45	Val	Tyr	Leu	Arg	Gln	Pro	Tyr	Tyr	Ala	Thr	Arg	Val	Asn	Ala	Ala	Asp
				210				215			220					
	Ile	Glu	Asn	Arg	Val	Leu	Glu	Leu	Asn	Lys	Lys	Gln	Glu	Ser	Glu	Asp
				225				230			235			240		
	Thr	Ala	Lys	Ala	Gly	Phe	Trp	Glu	Glu	Phe	Glu	Ser	Leu	Gln	Lys	Gln
				245				250			255					
50	Glu	Val	Lys	Asn	Leu	His	Gln	Arg	Leu	Glu	Gly	Gln	Arg	Pro	Glu	Asn
				260				265			270					
	Lys	Gly	Lys	Asn	Arg	Tyr	Lys	Asn	Ile	Leu	Pro	Phe	Asp	His	Ser	Arg
				275				280			285					
55	Val	Ile	Leu	Gln	Gly	Arg	Asp	Ser	Asn	Ile	Pro	Gly	Ser	Asp	Tyr	Ile
				290				295			300					
	Asn	Ala	Asn	Tyr	Ile	Lys	Asn	Gln	Leu	Leu	Gly	Pro	Asp	Glu	Asn	Ala

225

	305	310	315	320
	Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp			
	325	330	335	
5	Phe Trp Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr			
	340	345	350	
	Thr Arg Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro			
	355	360	365	
	Glu Val Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys			
	370	375	380	
10	Gly Glu His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser			
	385	390	395	400
	Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr			
	405	410	415	
	Leu Ser Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu			
15	420	425	430	
	Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala			
	435	440	445	
	Gly Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr			
	450	455	460	
20	Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu			
	465	470	475	480
	Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln			
	485	490	495	
	Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val			
25	500	505	510	
	Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu			
	515	520	525	
	Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro			
	530	535	540	
30	Pro Ala Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys			
	545	550	555	560
	His Lys Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu			
	565	570	575	
	Glu Lys Val Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly			
35	580	585	590	
	Ser Leu Lys Arg Lys Arg Ile Leu Gln Ser Thr Val Pro Arg Ala Arg			
	595	600	605	
	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr			
	610	615	620	
40	Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His			
	625	630	635	640
	Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys			
	645	650	655	
	Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp			
45	660	665	670	
	Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg			
	675	680	685	
	Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro			
	690	695	700	
50	Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn			
	705	710	715	720
	Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn			
	725	730	735	
	Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu			
55	740	745	750	
	Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met			

226

	755	760	765
	Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His		
	770	775	780
5	Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn		
	785	790	795
	Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu		800
	805	810	815
	Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His		
	820	825	830
10	Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met		
	835	840	845
	Asp Glu Leu Tyr Lys		
	850		

15 (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2994 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2991
 - (D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
35 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96		
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
40 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144		
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
45 TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192		
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
50 CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240		
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80
55 CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288		
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336		

226

227

	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100	105	110
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		384
	115	120	125
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		432
	130	135	140
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		480
	145	150	155
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		528
	165	170	175
20	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		576
	180	185	190
25	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		624
	195	200	205
30	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		672
	210	215	220
35	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		720
	225	230	235
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Glu Arg Pro		768
	245	250	255
40	CCG GGG CTG CGG CCG GGC GCG GGC GGG CCC TGG GAG ATG CGG GAG CGG Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu Met Arg Glu Arg		816
	260	265	270
45	CTG GGC ACC GGC GGC TTC GGG AAC GTC TGT CTG TAC CAG CAT CGG GAA Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr Gln His Arg Glu		864
	275	280	285
50	CTT GAT CTC AAA ATA GCA ATT AAG TCT TGT CGC CTA GAG CTA AGT ACC Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu Glu Leu Ser Thr		912
	290	295	300
55	AAA AAC AGA GAA CGA TGG TGC CAT GAA ATC CAG ATT ATG AAG AAG TTG Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile Met Lys Lys Leu		960
	305	310	315
	AAC CAT GCC AAT GTT GTA AAG GCC TGT GAT GTT CCT GAA GAA TTG AAT		1008

227

228

	Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro Glu Glu Leu Asn		
	325	330	335
5	ATT TTG ATT CAT GAT GTG CCT CTT CTA GCA ATG GAA TAC TGT TCT GGA Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu Tyr Cys Ser Gly		1056
	340	345	350
10	GGA GAT CTC CGA AAG CTG CTC AAC AAA CCA GAA AAT TGT TGT GGA CTT Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn Cys Cys Gly Leu		1104
	355	360	365
15	AAA GAA AGC CAG ATA CTT TCT TTA CTA AGT GAT ATA GGG TCT GGG ATT Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile Gly Ser Gly Ile		1152
	370	375	380
	CGA TAT TTG CAT GAA AAC AAA ATT ATA CAT CGA GAT CTA AAA CCT GAA Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp Leu Lys Pro Glu		1200
	385	390	395
20	AAC ATA GTT CTT CAG GAT GTT GGT GGA AAG ATA ATA CAT AAA ATA ATT Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile His Lys Ile Ile		1248
	405	410	415
25	GAT CTG GGA TAT GCC AAA GAT GTT GAT CAA GGA AGT CTG TGT ACA TCT Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser Leu Cys Thr Ser		1296
	420	425	430
30	TTT GTG GGA ACA CTG CAG TAT CTG GCC CCA GAG CTC TTT GAG AAT AAG Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu Phe Glu Asn Lys		1344
	435	440	445
35	CCT TAC ACA GCC ACT GTT GAT TAT TGG AGC TTT GGG ACC ATG GTA TTT Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly Thr Met Val Phe		1392
	450	455	460
	GAA TGT ATT GCT GGA TAT AGG CCT TTT TTG CAT CAT CTG CAG CCA TTT Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His Leu Gln Pro Phe		1440
	465	470	475
40	480	485	495
	ACC TGG CAT GAG AAG ATT AAG AAG AAG GAT CCA AAG TGT ATA TTT GCA Thr Trp His Glu Lys Ile Lys Lys Asp Pro Lys Cys Ile Phe Ala		1488
45	TGT GAA GAG ATG TCA GGA GAA GTT CGG TTT AGT AGC CAT TTA CCT CAA Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser His Leu Pro Gln		1536
	500	505	510
50	CCA AAT AGC CTT TGT AGT TTA ATA GTA GAA CCC ATG GAA AAC TGG CTA Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met Glu Asn Trp Leu		1584
	515	520	525
55	CAG TTG ATG TTG AAT TGG GAC CCT CAG CAG AGA GGA GGA CCT GTT GAC Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly Gly Pro Val Asp		1632
	530	535	540
	CTT ACT TTG AAG CAG CCA AGA TGT TTT GTA TTA ATG GAT CAC ATT TTG		1680

228

229

	Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met Asp His Ile Leu		
545	550	555	560
5	AAT TTG AAG ATA GTA CAC ATC CTA AAT ATG ACT TCT GCA AAG ATA ATT Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser Ala Lys Ile Ile		1728
	565	570	575
10	TCT TTT CTG TTA CCA CCT GAT GAA AGT CTT CAT TCA CTA CAG TCT CGT Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser Leu Gln Ser Arg		1776
	580	585	590
	ATT GAG CGT GAA ACT GGA ATA AAT ACT GGT TCT CAA GAA CTT CTT TCA Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln Glu Leu Leu Ser		1824
	595	600	605
15	GAG ACA GGA ATT TCT CTG GAT CCT CGG AAA CCA GCC TCT CAA TGT GTT Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala Ser Gln Cys Val		1872
	610	615	620
20	CTA GAT GGA GTT AGA GGC TGT GAT AGC TAT ATG GTT TAT TTG TTT GAT Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val Tyr Leu Phe Asp		1920
	625	630	635
25	AAA AGT AAA ACT GTA TAT GAA GGG CCA TTT GCT TCC AGA AGT TTA TCT Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser Arg Ser Leu Ser		1968
	645	650	655
30	GAT TGT GTA AAT TAT ATT GTA CAG GAC AGC AAA ATA CAG CTT CCA ATT Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile Gln Leu Pro Ile		2016
	660	665	670
	ATA CAG CTG CGT AAA GTG TGG GCT GAA GCA GTG CAC TAT GTG TCT GGA Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His Tyr Val Ser Gly		2064
	675	680	685
35	690	695	700
	CTA AAA GAA GAC TAT AGC AGG CTC TTT CAG GGA CAA AGG GCA GCA ATG Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln Arg Ala Ala Met		2112
	705	710	715
40	TTA AGT CTT CTT AGA TAT AAT GCT AAC TTA ACA AAA ATG AAG AAC ACT Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys Met Lys Asn Thr		2160
	720		
45	TTG ATC TCA GCA TCA CAA CAA CTG AAA GCT AAA TTG GAG TTT TTT CAC Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu Glu Phe Phe His		2208
	725	730	735
	AAA AGC ATT CAG CTT GAC TTG GAG AGA TAC AGC GAG CAG ATG ACG TAT Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu Gln Met Thr Tyr		2256
	740	745	750
50	GGG ATA TCT TCA GAA AAA ATG CTA AAA GCA TGG AAA GAA ATG GAA GAA Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys Glu Met Glu Glu		2304
	755	760	765
55	AAG GCC ATC CAC TAT GCT GAG GTT GGT GTC ATT GGA TAC CTG GAG GAT		2352

230

	Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly Tyr Leu Glu Asp		
	770	775	780
5	CAG ATT ATG TCT TTG CAT GCT GAA ATC ATG GGG CTA CAG AAG AGC CCC Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu Gln Lys Ser Pro		2400
	785	790	795
	800		
10	TAT GGA AGA CGT CAG GGA GAC TTG ATG GAA TCT CTG GAA CAG CGT GCC Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu Glu Gln Arg Ala		2448
	805	810	815
	815		
	ATT GAT CTA TAT AAG CAG TTA AAA CAC AGA CCT TCA GAT CAC TCC TAC Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser Asp His Ser Tyr		2496
	820	825	830
15	AGT GAC AGC ACA GAG ATG GTG AAA ATC ATT GTG CAC ACT GTG CAG AGT Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His Thr Val Gln Ser		2544
	835	840	845
20	CAG GAC CGT GTG CTC AAG GAG CTG TTT GGT CAT TTG AGC AAG TTG TTG Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu Ser Lys Leu Leu		2592
	850	855	860
25	GGC TGT AAG CAG AAG ATT ATT GAT CTA CTC CCT AAG GTG GAA GTG GCC Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys Val Glu Val Ala		2640
	865	870	875
	880		
30	CTC AGT AAT ATC AAA GAA GCT GAC AAT ACT GTC ATG TTC ATG CAG GGA Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met Phe Met Gln Gly		2688
	885	890	895
	895		
	AAA AGG CAG AAA GAA ATA TGG CAT CTC CTT AAA ATT GCC TGT ACA CAG Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile Ala Cys Thr Gln		2736
	900	905	910
35	AGT TCT GCC CGC TCT CTT GTA GGA TCC AGT CTA GAA GGT GCA GTA ACC Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu Gly Ala Val Thr		2784
	915	920	925
40	CCT CAG ACA TCA GCA TGG CTG CCC CCG ACT TCA GCA GAA CAT GAT CAT Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala Glu His Asp His		2832
	930	935	940
45	TCT CTG TCA TGT GTG GTA ACT CCT CAA GAT GGG GAG ACT TCA GCA CAA Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu Thr Ser Ala Gln		2880
	945	950	955
	960		
50	ATG ATA GAA GAA AAT TTG AAC TGC CTT GCC CAT TTA AGC ACT ATT ATT Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu Ser Thr Ile Ile		2928
	965	970	975
	975		
	CAT GAG GCA AAT GAG GAA CAG GGC AAT AGT ATG ATG AAT CTT GAT TGG His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met Asn Leu Asp Trp		2976
	980	985	990
55	AGT TGG TTA ACA GAA TGA		2994
	990		
	230		

Ser Trp Leu Thr Glu
995

5 (2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
20 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
25 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
30 Arg Thr Ile Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
35 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
40 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
180	185	190	
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
45 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
210	215	220	
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
225	230	235	240
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Glu Arg Pro			
245	250	255	
50 Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu Met Arg Glu Arg			
260	265	270	
Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr Gln His Arg Glu			
275	280	285	
55 Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu Glu Leu Ser Thr			
290	295	300	
Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile Met Lys Lys Leu			

232

	305	310	315	320
	Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro Glu Glu Leu Asn			
	325	330	335	
5	Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu Tyr Cys Ser Gly			
	340	345	350	
	Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn Cys Cys Gly Leu			
	355	360	365	
	Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile Gly Ser Gly Ile			
	370	375	380	
10	Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp Leu Lys Pro Glu			
	385	390	395	400
	Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile His Lys Ile Ile			
	405	410	415	
15	Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser Leu Cys Thr Ser			
	420	425	430	
	Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu Phe Glu Asn Lys			
	435	440	445	
	Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly Thr Met Val Phe			
	450	455	460	
20	Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His Leu Gln Pro Phe			
	465	470	475	480
	Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys Cys Ile Phe Ala			
	485	490	495	
25	Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser His Leu Pro Gln			
	500	505	510	
	Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met Glu Asn Trp Leu			
	515	520	525	
	Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly Gly Pro Val Asp			
	530	535	540	
30	Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met Asp His Ile Leu			
	545	550	555	560
	Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser Ala Lys Ile Ile			
	565	570	575	
35	Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser Leu Gln Ser Arg			
	580	585	590	
	Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln Glu Leu Leu Ser			
	595	600	605	
	Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala Ser Gln Cys Val			
	610	615	620	
40	Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val Tyr Leu Phe Asp			
	625	630	635	640
	Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser Arg Ser Leu Ser			
	645	650	655	
45	Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile Gln Leu Pro Ile			
	660	665	670	
	Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His Tyr Val Ser Gly			
	675	680	685	
	Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln Arg Ala Ala Met			
	690	695	700	
50	Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys Met Lys Asn Thr			
	705	710	715	720
	Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu Glu Phe Phe His			
	725	730	735	
55	Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu Gln Met Thr Tyr			
	740	745	750	
	Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys Glu Met Glu Glu			

233

	755	760	765
	Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly Tyr Leu Glu Asp		
	770	775	780
5	Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu Gln Lys Ser Pro		
	785	790	795
	Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu Glu Gln Arg Ala		800
	805	810	815
10	Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser Asp His Ser Tyr		
	820	825	830
	Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His Thr Val Gln Ser		
	835	840	845
	Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu Ser Lys Leu Leu		
	850	855	860
15	Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys Val Glu Val Ala		
	865	870	875
	Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met Phe Met Gln Gly		
	885	890	895
	Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile Ala Cys Thr Gln		
	900	905	910
20	Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu Gly Ala Val Thr		
	915	920	925
	Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala Glu His Asp His		
	930	935	940
	Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu Thr Ser Ala Gln		
25	945	950	955
	Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu Ser Thr Ile Ile		
	965	970	975
	His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met Asn Leu Asp Trp		
	980	985	990
30	Ser Trp Leu Thr Glu		
	995		

(2) INFORMATION FOR SEQ ID NO:122:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2991 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: cDNA	
	(ix) FEATURE:	
	(A) NAME/KEY: Coding Sequence	
45	(B) LOCATION: 1...2988	
	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
50	ATG GAG CGG CCC CCG GGG CTG CGG CCG GGC GCG GGC GGG CCC TGG GAG	48
	Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu	
	1 5 10 15	
55	ATG CGG GAG CGG CTG GGC ACC GGC GGC TTC GGG AAC GTC TGT CTG TAC	96
	Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr	
	20 25 30	

233

234

	CAG CAT CGG GAA CTT GAT CTC AAA ATA GCA ATT AAG TCT TGT CGC CTA Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu 35 40 45	144
5	GAG CTA AGT ACC AAA AAC AGA GAA CGA TGG TGC CAT GAA ATC CAG ATT Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile 50 55 60	192
10	ATG AAG AAG TTG AAC CAT GCC AAT GTT GTA AAG GCC TGT GAT GTT CCT Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro 65 70 75 80	240
15	GAA GAA TTG AAT ATT TTG ATT CAT GAT GTG CCT CTT CTA GCA ATG GAA Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu 85 90 95	288
20	TAC TGT TCT GGA GGA GAT CTC CGA AAG CTG CTC AAC AAA CCA GAA AAT Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn 100 105 110	336
25	TGT TGT GGA CTT AAA GAA AGC CAG ATA CTT TCT TTA CTA AGT GAT ATA Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile 115 120 125	384
30	GGG TCT GGG ATT CGA TAT TTG CAT GAA AAC AAA ATT ATA CAT CGA GAT Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp 130 135 140	432
35	CTA AAA CCT GAA AAC ATA GTT CTT CAG GAT GTT GGT GGA AAG ATA ATA Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile 145 150 155 160	480
40	CAT AAA ATA ATT GAT CTG GGA TAT GCC AAA GAT GTT GAT CAA GGA AGT His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser 165 170 175	528
45	CTG TGT ACA TCT TTT GTG GGA ACA CTG CAG TAT CTG GCC CCA GAG CTC Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu 180 185 190	576
50	TTT GAG AAT AAG CCT TAC ACA GCC ACT GTT GAT TAT TGG AGC TTT GGG Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly 195 200 205	624
55	ACC ATG GTA TTT GAA TGT ATT GCT GGA TAT AGG CCT TTT TTG CAT CAT Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His 210 215 220	672
55	CTG CAG CCA TTT ACC TGG CAT GAG AAG ATT AAG AAG AAG GAT CCA AAG Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys 225 230 235 240	720
55	TGT ATA TTT GCA TGT GAA GAG ATG TCA GGA GAA GTT CGG TTT AGT AGC Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser 245 250 255	768

234

235

	CAT TTA CCT CAA CCA AAT AGC CTT TGT AGT TTA ATA GTA GAA CCC ATG His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met 260 265 270	816
5	GAA AAC TGG CTA CAG TTG ATG TTG AAT TGG GAC CCT CAG CAG AGA GGA Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly 275 280 285	864
10	GGA CCT GTT GAC CTT ACT TTG AAG CAG CCA AGA TGT TTT GTA TTA ATG Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met 290 295 300	912
15	GAT CAC ATT TTG AAT TTG AAG ATA GTA CAC ATC CTA AAT ATG ACT TCT Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser 305 310 315 320	960
20	GCA AAG ATA ATT TCT TTT CTG TTA CCA CCT GAT GAA AGT CTT CAT TCA Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser 325 330 335	1008
25	CTA CAG TCT CGT ATT GAG CGT GAA ACT GGA ATA AAT ACT GGT TCT CAA Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln 340 345 350	1056
30	GAA CTT CTT TCA GAG ACA GGA ATT TCT CTG GAT CCT CGG AAA CCA GCC Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala 355 360 365	1104
35	TCT CAA TGT GTT CTA GAT GGA GTT AGA GGC TGT GAT AGC TAT ATG GTT Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val 370 375 380	1152
40	TAT TTG TTT GAT AAA AGT AAA ACT GTA TAT GAA GGG CCA TTT GCT TCC Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser 385 390 395 400	1200
45	AGA AGT TTA TCT GAT TGT GTA AAT TAT ATT GTA CAG GAC AGC AAA ATA Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile 405 410 415	1248
50	CAG CTT CCA ATT ATA CAG CTG CGT AAA GTG TGG GCT GAA GCA GTG CAC Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His 420 425 430	1296
55	TAT GTG TCT GGA CTA AAA GAA GAC TAT AGC AGG CTC TTT CAG GGA CAA Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln 435 440 445	1344
50	AGG GCA GCA ATG TTA AGT CTT CTT AGA TAT AAT GCT AAC TTA ACA AAA Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys 450 455 460	1392
55	ATG AAG AAC ACT TTG ATC TCA GCA TCA CAA CAA CTG AAA GCT AAA TTG Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu 465 470 475 480	1440

	GAG TTT TTT CAC AAA AGC ATT CAG CTT GAC TTG GAG AGA TAC AGC GAG Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu 485 490 495	1488
5	CAG ATG ACG TAT GGG ATA TCT TCA GAA AAA ATG CTA AAA GCA TGG AAA Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys 500 505 510	1536
10	GAA ATG GAA GAA AAG GCC ATC CAC TAT GCT GAG GTT GGT GTC ATT GGA Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly 515 520 525	1584
15	TAC CTG GAG GAT CAG ATT ATG TCT TTG CAT GCT GAA ATC ATG GGG CTA Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu 530 535 540	1632
20	CAG AAG AGC CCC TAT GGA AGA CGT CAG GGA GAC TTG ATG GAA TCT CTG Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu 545 550 555 560	1680
25	GAA CAG CGT GCC ATT GAT CTA TAT AAG CAG TTA AAA CAC AGA CCT TCA Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser 565 570 575	1728
30	GAT CAC TCC TAC AGT GAC AGC ACA GAG ATG GTG AAA ATC ATT GTG CAC Asp His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His 580 585 590	1776
35	ACT GTG CAG AGT CAG GAC CGT GTG CTC AAG GAG CTG TTT GGT CAT TTG Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu 595 600 605	1824
40	AGC AAG TTG TTG GGC TGT AAG CAG AAG ATT ATT GAT CTA CTC CCT AAG Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys 610 615 620	1872
45	GTG GAA GTG GCC CTC AGT AAT ATC AAA GAA GCT GAC AAT ACT GTC ATG Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met 625 630 635 640	1920
50	TTC ATG CAG GGA AAA AGG CAG AAA GAA ATA TGG CAT CTC CTT AAA ATT Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile 645 650 655	1968
55	GCC TGT ACA CAG AGT TCT GCC CGC TCT CTT GTA GGA TCC AGT CTA GAA Ala Cys Thr Gln Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu 660 665 670	2016
60	GGT GCA GTA ACC CCT CAG ACA TCA GCA TGG CTG CCC CCG ACT TCA GCA Gly Ala Val Thr Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala 675 680 685	2064
65	GAA CAT GAT CAT TCT CTG TCA TGT GTG GTA ACT CCT CAA GAT GGG GAG Glu His Asp His Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu 690 695 700	2112

	ACT TCA GCA CAA ATG ATA GAA GAA AAT TTG AAC TGC CTT GGC CAT TTA Thr Ser Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu 705 710 715 720	2160
5	AGC ACT ATT ATT CAT GAG GCA AAT GAG GAA CAG GGC AAT AGT ATG ATG Ser Thr Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met 725 730 735	2208
10	AAT CTT GAT TGG AGT TGG TTA ACA GAA TGG GTA CCG CGG GCC CGG GAT Asn Leu Asp Trp Ser Trp Leu Thr Glu Trp Val Pro Arg Ala Arg Asp 740 745 750	2256
15	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly 755 760 765	2304
20	GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys 770 775 780	2352
25	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG Phe Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu 785 790 795 800	2400
30	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro 805 810 815	2448
35	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr 820 825 830	2496
40	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu 835 840 845	2544
45	GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr 850 855 860	2592
50	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg 865 870 875 880	2640
55	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly 885 890 895	2688
50	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala 900 905 910	2736
55	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn 915 920 925	2784

	ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr 930 935 940	2832
5	CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser 945 950 955 960	2880
10	ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met 965 970 975	2928
15	GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp 980 985 990	2976
20	GAG CTG TAC AAG TAA Glu Leu Tyr Lys 995	2991

(2) INFORMATION FOR SEQ ID NO:123:

25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 996 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
30	(ii) MOLECULE TYPE: protein (v) FRAGMENT TYPE: internal
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123: Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu 1 5 10 15 Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr 20 25 30 40 Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu 35 40 45 Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile 50 55 60 45 Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro 65 70 75 80 Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu 85 90 95 Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn 100 105 110 50 Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile 115 120 125 Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp 130 135 140 55 Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile 145 150 155 160 His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser

239

	165	170	175
	Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu		
	180	185	190
5	Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly		
	195	200	205
	Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His		
	210	215	220
	Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys		
	225	230	235
10		240	
	Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser		
	245	250	255
	His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met		
	260	265	270
15	Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly		
	275	280	285
	Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met		
	290	295	300
	Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser		
	305	310	315
20		320	
	Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser		
	325	330	335
	Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln		
	340	345	350
25	Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala		
	355	360	365
	Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val		
	370	375	380
	Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser		
	385	390	395
30		400	
	Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile		
	405	410	415
	Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His		
	420	425	430
35	Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln		
	435	440	445
	Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys		
	450	455	460
	Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu		
	465	470	475
40		480	
	Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu		
	485	490	495
	Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys		
	500	505	510
45			
	Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly		
	515	520	525
	Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu		
	530	535	540
	Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu		
	545	550	555
50		560	
	Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser		
	565	570	575
	Asp His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His		
	580	585	590
55			
	Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu		
	595	600	605
	Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys		

240

	610	615	620
	Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met		
5	625	630	635
	Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile		640
	645	650	655
	Ala Cys Thr Gln Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu		
	660	665	670
10	Gly Ala Val Thr Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala		
	675	680	685
	Glu His Asp His Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu		
	690	695	700
	Thr Ser Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu		
	705	710	715
15	Ser Thr Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met		720
	725	730	735
	Asn Leu Asp Trp Ser Trp Leu Thr Glu Trp Val Pro Arg Ala Arg Asp		
	740	745	750
	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly		
	755	760	765
20	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys		
	770	775	780
	Phe Ser Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu		
	785	790	795
25	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro		800
	805	810	815
	Thr Leu Val Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr		
	820	825	830
	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu		
	835	840	845
30	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr		
	850	855	860
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg		
	865	870	875
35	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly		880
	885	890	895
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala		
	900	905	910
	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn		
	915	920	925
40	Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr		
	930	935	940
	Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser		
	945	950	955
45	Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met		960
	965	970	975
	Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp		
	980	985	990
	Glu Leu Tyr Lys		
50	995		

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

241

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

5

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1905
(D) OTHER INFORMATION:

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
15	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
30	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
35	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
40	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
50	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
55	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576

241

242

	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
	180	185	190
5	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		624
	195	200	205
10	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		672
	210	215	220
	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		720
	225	230	235
15	Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met GGA CTC AGA TCT CGA GCT CAA GCT TCC ATG AGC GAG ACG GTC ATC ATG		768
	245	250	255
20	Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met AGC GAG ACG GTC ATC TGT TCC AGC CGG GCC ACT GTG ATG CTT TAT GAT		816
	Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp		
	260	265	270
25	GAT GGC AAC AAG CGA TGG CTC CCT GCT GGC ACG GGT CCC CAG GCC TTC Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe		864
	275	280	285
30	AGC CGC GTC CAG ATC TAC CAC AAC CCC ACG GCC AAT TCC TTT CGC GTC Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val		912
	290	295	300
35	GTG GGC CGG AAG ATG CAG CCC GAC CAG CAG GTG GTC ATC AAC TGT GCC Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala		960
	305	310	315
	320		
	ATC GTC CGG GGT GTC AAG TAT AAC CAG GCC ACC CCC AAC TTC CAT CAG Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln		1008
	325	330	335
40	TGG CGC GAC GCT CGC CAG GTC TGG GGC CTC AAC TTC GGC AGC AAG GAG Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu		1056
	340	345	350
45	GAT GCG GCC CAG TTT GCC GCC GGC ATG GCC AGT GCC CTA GAG GCG TTG Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu		1104
	355	360	365
50	GAA GGA GGT GGG CCC CCT CCA CCC CCA GCA CTT CCC ACC TGG TCG GTC Glu Gly Gly Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val		1152
	370	375	380
55	CCG AAC GGC CCC TCC CCG GAG GAG GTG GAG CAG CAG AAA AGG CAG CAG Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln		1200
	385	390	395
	400		
	CCC GGC CCG TCG GAG CAC ATA GAG CGC CGG GTC TCC AAT GCA GGA GGC		1248

242

243

	Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly		
	405	410	415
5	CCA CCT GCT CCC CCC GCT GGG GGT CCA CCC CCA CCA GGA CCT CCC Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro		1296
	420	425	430
10	CCT CCT CCA GGT CCC CCC CCA CCC CCA GGT TTG CCC CCT TCG GGG GTC Pro Pro Pro Gly Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val		1344
	435	440	445
	CCA GCT GCA GCG CAC GGA GCA GGG GGA GGA CCA CCC CCT GCA CCC CCT Pro Ala Ala Ala His Gly Ala Gly Gly Pro Pro Pro Ala Pro Pro		1392
15	450	455	460
	CTC CCG GCA GCA CAG GGC CCT GGT GGT GGG GGA GCT GGG GCC CCA GGC Leu Pro Ala Ala Gln Gly Pro Gly Gly Ala Gly Ala Pro Gly		1440
	465	470	475
20	CTG GCC GCA GCT ATT GCT GGA GCC AAA CTC AGG AAA GTC AGC AAG CAG Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln		1488
	485	490	495
25	GAG GAG GCC TCA GGG GGG CCC ACA GCC CCC AAA GCT GAG AGT GGT CGA Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg		1536
	500	505	510
30	AGC GGA GGT GGG GGA CTC ATG GAA GAG ATG AAC GCC ATG CTG GCC CGG Ser Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg		1584
	515	520	525
	AGA AGG AAA GCC ACG CAA GTT GGG GAG AAA ACC CCC AAG GAT GAA TCT Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser		1632
35	530	535	540
	GCC AAT CAG GAG GAG CCA GAG GCC AGA GTC CCG GCC CAG AGT GAA TCT Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser		1680
	545	550	555
40	GTG CGG AGA CCC TGG GAG AAG AAC AGC ACA ACC TTG CCA AGG ATG AAG Val Arg Arg Pro Trp Glu Lys Asn Ser Thr Thr Leu Pro Arg Met Lys		1728
	565	570	575
45	TCG TCT TCG GTG ACC ACT TCC GAG ACC CAA CCC TGC ACG CCC AGC Ser Ser Ser Val Thr Thr Ser Glu Thr Gln Pro Cys Thr Pro Ser		1776
	580	585	590
50	TCC AGT GAT TAC TCG GAC CTA CAG AGG GTG AAA CAG GAG CTT CTG GAA Ser Ser Asp Tyr Ser Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu		1824
	595	600	605
	GAG GTG AAG AAG GAA TTG CAG AAA GTG AAA GAG GAA ATC ATT GAA GCC Glu Val Lys Lys Glu Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala		1872
55	610	615	620
	TTC GTC CAG GAG CTG AGG AAG CGG GGT TCT CCC TGA		1908

244

Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro
 625 630 635

5 (2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
30	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
40	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
45	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met	
	245 250 255	
50	Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp	
	260 265 270	
	Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe	
	275 280 285	
	Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val	
55	290 295 300	
	Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala	

245

305	310	315	320
Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln			
325	330	335	
Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu			
340	345	350	
Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu			
355	360	365	
Glu Gly Gly Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val			
370	375	380	
10 Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln			
385	390	395	400
Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly			
405	410	415	
Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Gly Pro Pro			
420	425	430	
Pro Pro Pro Gly Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val			
435	440	445	
Pro Ala Ala Ala His Gly Ala Gly Gly Pro Pro Pro Ala Pro Pro			
450	455	460	
20 Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Ala Gly Ala Pro Gly			
465	470	475	480
Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln			
485	490	495	
Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg			
500	505	510	
Ser Gly Gly Gly Leu Met Glu Met Asn Ala Met Leu Ala Arg			
515	520	525	
Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser			
530	535	540	
30 Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser			
545	550	555	560
Val Arg Arg Pro Trp Glu Lys Asn Ser Thr Thr Leu Pro Arg Met Lys			
565	570	575	
Ser Ser Ser Ser Val Thr Thr Ser Glu Thr Gln Pro Cys Thr Pro Ser			
580	585	590	
Ser Ser Asp Tyr Ser Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu			
595	600	605	
Glu Val Lys Lys Glu Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala			
610	615	620	
40 Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro			
625	630	635	

(2) INFORMATION FOR SEQ ID NO:126:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1326
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

5	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
65	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672

247

	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
	210	215	220
5	GTC ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		720
	225	230	235
10	GGA CTC AGA TCT CGA GCT CAA GCT TCA ATG GCT GCC ATC CGG AAG AAA Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ala Ala Ile Arg Lys Lys		768
	245	250	255
	CTG GTG ATT GTT GGT GAT GGA GCC TGT GGA AAG ACA TGC TTG CTC ATA Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile		816
	260	265	270
15	GTC TTC AGC AAG GAC CAG TTC CCA GAG GTG TAT GTG CCC ACA GTG TTT Val Phe Ser Lys Asp Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe		864
	275	280	285
20	GAG AAC TAT GTG GCA GAT ATC GAG GTG GAT GGA AAG CAG GTA GAG TTG Glu Asn Tyr Val Ala Asp Ile Glu Val Asp Gly Lys Gln Val Glu Leu		912
	290	295	300
25	GCT TTG TGG GAC ACA GCT GGG CAG GAA GAT TAT GAT CGC CTG AGG CCC Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro		960
	305	310	315
30	320	325	330
	CTC TCC TAC CCA GAT ACC GAT GTT ATA CTG ATG TGT TTT TCC ATC GAC Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp		1008
	335		
	AGC CCT GAT AGT TTA GAA AAC ATC CCA GAA AAG TGG ACC CCA GAA GTC Ser Pro Asp Ser Leu Glu Asn Ile Pro Glu Lys Trp Thr Pro Glu Val		1056
	340	345	350
35	AAG CAT TTC TGT CCC AAC GTG CCC ATC ATC CTG GTT GGG AAT AAG AAG Lys His Phe Cys Pro Asn Val Pro Ile Ile Leu Val Gly Asn Lys Lys		1104
	355	360	365
40	GAT CTT CGG AAT GAT GAG CAC ACA AGG CGG GAG CTA GCC AAG ATG AAG Asp Leu Arg Asn Asp Glu His Thr Arg Arg Glu Leu Ala Lys Met Lys		1152
	370	375	380
45	CAG GAG CCG GTG AAA CCT GAA GAA GGC AGA GAT ATG GCA AAC AGG ATT Gln Glu Pro Val Lys Pro Glu Glu Gly Arg Asp Met Ala Asn Arg Ile		1200
	385	390	395
50	400	405	410
	GGC GCT TTT GGG TAC ATG GAG TGT TCA GCA AAG ACC AAA GAT GGA GTG Gly Ala Phe Gly Tyr Met Glu Cys Ser Ala Lys Thr Lys Asp Gly Val		1248
	415		
	AGA GAG GTT TTT GAA ATG GCT ACG AGA GCT GCT CTG CAA GCT AGA CGT Arg Glu Val Phe Glu Met Ala Thr Arg Ala Ala Leu Gln Ala Arg Arg		1296
	420	425	430
55	GGG AAG AAA AAA TCT GGT TGC CTT GTC TTG TGA		1329

247

248

Gly Lys Lys Lys Ser Gly Cys Leu Val Leu
 435 440

5 (2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
				20				25						30		
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Ieu	Lys	Phe	Ile
					35				40					45		
25	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
					50			55			60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
30					65			70		75				80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
					85				90					95		
35	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
					100			105			110					
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
40					115			120			125					
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Ieu	Glu	Tyr
					130			135			140					
45	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
					145			150			155			160		
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
					165				170			175				
50	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
					180			185			190					
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
					195			200			205					
55	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
					210			215			220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
					225			230			235			240		
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ala	Ala	Ile	Arg	Lys	Lys
					245				250					255		
60	Leu	Val	Ile	Val	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile
					260			265			270					
	Val	Phe	Ser	Lys	Asp	Gln	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe
					275			280			285					
	Glu	Asn	Tyr	Val	Ala	Asp	Ile	Glu	Val	Asp	Gly	Lys	Gln	Val	Glu	Leu
					290			295			300					
	Ala	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro

248

249

	305	310	315	320
	Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp			
	325	330	335	
5	Ser Pro Asp Ser Leu Glu Asn Ile Pro Glu Lys Trp Thr Pro Glu Val			
	340	345	350	
	Lys His Phe Cys Pro Asn Val Pro Ile Ile Leu Val Gly Asn Lys Lys			
	355	360	365	
	Asp Leu Arg Asn Asp Glu His Thr Arg Arg Glu Leu Ala Lys Met Lys			
10	370	375	380	
	Gln Glu Pro Val Lys Pro Glu Glu Gly Arg Asp Met Ala Asn Arg Ile			
	385	390	395	400
	Gly Ala Phe Gly Tyr Met Glu Cys Ser Ala Lys Thr Lys Asp Gly Val			
	405	410	415	
15	Arg Glu Val Phe Glu Met Ala Thr Arg Ala Ala Leu Gln Ala Arg Arg			
	420	425	430	
	Gly Lys Lys Lys Ser Gly Cys Leu Val Leu			
	435	440		

(2) INFORMATION FOR SEQ ID NO:128:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
 30 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1137
 (D) OTHER INFORMATION:

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

	ATG GAC CAT TAT GAT TCT CAG CAA ACC AAC GAT TAC ATG CAG CCA GAA		48
	Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu		
	1 5 10 15		
40	GAG GAC TGG GAC CGG GAC CTG CTC CTG GAC CCG GCC TGG GAG AAG CAG		96
	Glu Asp Trp Asp Arg Asp Leu Leu Asp Pro Ala Trp Glu Lys Gln		
	20 25 30		
45	CAG AGA AAG ACA TTC ACG GCA TGG TGT AAC TCC CAC CTC CGG AAG GCG		144
	Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala		
	35 40 45		
50	GGG ACA CAG ATC GAG AAC ATC GAA GAG GAC TTC CGG GAT GGC CTG AAG		192
	Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys		
	50 55 60		
55	CTC ATG CTG CTG GAG GTC ATC TCA GGT GAA CGC TTG GCC AAG CCA		240
	Leu Met Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro		
	65 70 75 80		
	GAG CGA GGC AAG ATG AGA GTG CAC AAG ATC TCC AAC GTC AAC AAG GCC		288

249

250

	Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala		
	85	90	95
5	CTG GAT TTC ATA GCC AGC AAA GGC GTC AAA CTG GTG TCC ATC GGA GCC Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala		336
	100	105	110
10	GAA GAA ATC GTG GAT GGG AAT GTG AAG ATG ACC CTG GGC ATG ATC TGG Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp		384
	115	120	125
15	ACC ATC ATC CTG CGC AGG GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG Thr Ile Ile Leu Arg Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys		432
	130	135	140
20	GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG GAC Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp		480
	145	150	155
	160		
25	GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly		528
	165	170	175
30	GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly		576
	180	185	190
35	AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly		624
	195	200	205
40	GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe		672
	210	215	220
45	TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe		720
	225	230	235
	240		
50	TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu		768
	245	250	255
55	GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys		816
	260	265	270
60	GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser		864
	275	280	285
65	CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val		912
	290	295	300
70	AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC		960
			250

251

	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala		
305	310	315	320
5	GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG		1008
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu		
	325	330	335
10	CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC		1056
	Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro		
	340	345	350
15	AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC		1104
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala		
	355	360	365
	GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA		1140
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	370	375	

20

(2) INFORMATION FOR SEQ ID NO:129:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 379 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: protein	
	(v) FRAGMENT TYPE: internal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:	
35	Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu	
	1 5 10 15	
	Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln	
	20 25 30	
	Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala	
	35 40 45	
40	Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys	
	50 55 60	
	Leu Met Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro	
	65 70 75 80	
	Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala	
45	85 90 95	
	Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala	
	100 105 110	
	Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp	
	115 120 125	
50	Thr Ile Ile Leu Arg Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys	
	130 135 140	
	Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp	
	145 150 155 160	
	Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly	
55	165 170 175	
	Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly	

252

	180	185	190
	Lys Leu Pro Val Pro Trp Pro Thr	Leu Val Thr Thr	Leu Thr Tyr Gly
	195	200	205
5	Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe		
	210	215	220
	Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe		
	225	230	235
	Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu		240
	245	250	255
10	Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys		
	260	265	270
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser		
	275	280	285
15	His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val		
	290	295	300
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala		
	305	310	315
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu		320
	325	330	335
20	Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro		
	340	345	350
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala		
	355	360	365
25	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	370	375	

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 3516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:
- 40 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...3513
 (D) OTHER INFORMATION:
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:
- | | | |
|----|---|-----|
| | ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG | 48 |
| 45 | Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| | 1 5 10 15 | |
| | GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC | 96 |
| 50 | Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| | 20 25 30 | |
| | GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC | 144 |
| | Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile | |
| | 35 40 45 | |
| 55 | TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC | 192 |

252

253

	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60	
5	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	240	
65	70	75	80
10	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288	
85	90	95	
15	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336	
100	105	110	
20	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384	
115	120	125	
25	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432	
130	135	140	
30	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480	
145	150	155	160
35	GGC ATC AAG GTG AAC TTC AAG ATC CCG CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	528	
165	170	175	
40	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	576	
180	185	190	
45	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	624	
195	200	205	
50	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	672	
210	215	220	
55	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	720	
225	230	235	240
55	GGA CTC AGA TCT CGA GCC ATG AAC GCC CCC GAG CGG CAG CCC CAA CCC Gly Leu Arg Ser Arg Ala Met Asn Ala Pro Glu Arg Gln Pro Gln Pro	768	
245	250	255	
55	GAC GGC GGG GAC GCC CCA GGC CAC GAG CCT GGG GGC AGC CCC CAA GAC Asp Gly Asp Ala Pro Gly His Glu Pro Gly Gly Ser Pro Gln Asp	816	
260	265	270	
55	GAG CTT GAC TTC TCC ATC CTC TTC GAC TAT GAG TAT TTG AAT CCG AAC	864	
		253	

254

	Glu Leu Asp Phe Ser Ile Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn		
	275	280	285
5	GAA GAA GAG CCG AAT GCA CAT AAG GTC GCC AGC CCA CCC TCC GGA CCC Glu Glu Glu Pro Asn Ala His Lys Val Ala Ser Pro Pro Ser Gly Pro		912
	290	295	300
10	GCA TAC CCC GAT GAT GTA ATG GAC TAT GGC CTC AAG CCA TAC AGC CCC Ala Tyr Pro Asp Asp Val Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro		960
	305	310	315
	320		
	CTT GCT AGT CTC TCT GGC GAG CCC CCC GGC CGA TTC GGA GAG CCG GAT Leu Ala Ser Leu Ser Gly Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp		1008
	325	330	335
15	AGG GTA GGG CCG CAG AAG TTT CTG AGC GCG GCC AAG CCA GCA GGG GCC Arg Val Gly Pro Gln Lys Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala		1056
	340	345	350
20	TCG GGC CTG AGC CCT CCG ATC GAG ATC ACT CCG TCC CAC GAA CTG ATC Ser Gly Leu Ser Pro Arg Ile Glu Ile Thr Pro Ser His Glu Leu Ile		1104
	355	360	365
25	CAG GCA GTG GGG CCC CTC CGC ATG AGA GAC GCG GGC CTC CTG GTG GAG Gln Ala Val Gly Pro Leu Arg Met Arg Asp Ala Gly Leu Leu Val Glu		1152
	370	375	380
30	CAG CCT CCC CTG GCC GGG GTG GCC AGC CCG AGG TTC ACC CTG CCC Gln Pro Pro Leu Ala Gly Val Ala Ala Ser Pro Arg Phe Thr Leu Pro		1200
	385	390	395
	400		
	GTG CCC GGC TTC GAG GGC TAC CGC GAG CCG CTT TGC TTG AGC CCC GCT Val Pro Gly Phe Glu Gly Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala		1248
35	405	410	415
	AGC AGC GGC TCC TCT GCC AGC TTC ATT TCT GAC ACC TTC TCC CCC TAC Ser Ser Gly Ser Ser Ala Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr		1296
	420	425	430
40	ACC TCG CCC TGC TCG CCC AAT AAC GGC GGG CCC GAC GAC CTG TGT Thr Ser Pro Cys Val Ser Pro Asn Asn Gly Pro Asp Asp Leu Cys		1344
	435	440	445
45	CCG CAG TTT CAA AAC ATC CCT GCT CAT TAT TCC CCC AGA ACC TCG CCA Pro Gln Phe Gln Asn Ile Pro Ala His Tyr Ser Pro Arg Thr Ser Pro		1392
	450	455	460
50	ATA ATG TCA CCT CGA ACC AGC CTC GCC GAG GAC AGC TGC CTG GGC CGC Ile Met Ser Pro Arg Thr Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg		1440
	465	470	475
	480		
	CAC TCG CCC GTG CCC CGT CCG GCC TCC CGC TCC TCA TCG CCT GGT GCC His Ser Pro Val Pro Arg Pro Ala Ser Arg Ser Ser Pro Gly Ala		1488
	485	490	495
55	AAG CGG AGG CAT TCG TGC GCC GAG GCC TTG GTT GCC CTG CCG CCC GGA		1536
	254		

255

	Lys Arg Arg His Ser Cys Ala Glu Ala Leu Val Ala Leu Pro Pro Gly		
	500	505	510
5	GCC TCA CCC CAG CGC TCC CGG AGC CCC TCG CCG CAG CCC TCA TCT CAC Ala Ser Pro Gln Arg Ser Arg Ser Pro Ser Pro Gln Pro Ser Ser His		1584
	515	520	525
10	GTG GCA CCC CAG GAC CAC GGC TCC CCG GCT GGG TAC CCC CCT GTG GCT Val Ala Pro Gln Asp His Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala		1632
	530	535	540
15	GGC TCT GCC GTG ATC ATG GAT GCC CTG AAC AGC CTC GCC ACG GAC TCG Gly Ser Ala Val Ile Met Asp Ala Leu Asn Ser Leu Ala Thr Asp Ser		1680
	545	550	555
	CCT TGT GGG ATC CCC CCC AAG ATG TGG AAG ACC AGC CCT GAC CCC TCG Pro Cys Gly Ile Pro Pro Lys Met Trp Lys Thr Ser Pro Asp Pro Ser		1728
	565	570	575
20	CCG GTG TCT GCC GCC CCA TCC AAG GCC GGC CTG CCT CGC CAC ATC TAC Pro Val Ser Ala Ala Pro Ser Lys Ala Gly Leu Pro Arg His Ile Tyr		1776
	580	585	590
25	CCG GCC GTG GAG TTC CTG GGG CCC TGC GAG CAG GGC GAG AGG AGA AAC Pro Ala Val Glu Phe Leu Gly Pro Cys Glu Gln Gly Glu Arg Arg Asn		1824
	595	600	605
30	TCG GCT CCA GAA TCC ATC CTG CTG GTT CCG CCC ACT TGG CCC AAG CCG Ser Ala Pro Glu Ser Ile Leu Leu Val Pro Pro Thr Trp Pro Lys Pro		1872
	610	615	620
35	CTG GTG CCT GCC ATT CCC ATC TGC AGC ATC CCA GTG ACT GCA TCC CTC Leu Val Pro Ala Ile Pro Ile Cys Ser Ile Pro Val Thr Ala Ser Leu		1920
	625	630	635
	CCT CCA CTT GAG TGG CCG CTG TCC AGT CAG TCA GGC TCT TAC GAG CTG Pro Pro Leu Glu Trp Pro Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu		1968
	645	650	655
40	CGG ATC GAG GTG CAG CCC AAG CCA CAT CAC CGG GCC CAC TAT GAG ACA Arg Ile Glu Val Gln Pro Lys Pro His His Arg Ala His Tyr Glu Thr		2016
	660	665	670
45	GAA GGC AGC CGA GGG GCT GTC AAA GCT CCA ACT GGA GGC CAC CCT GTG Glu Gly Ser Arg Gly Ala Val Lys Ala Pro Thr Gly Gly His Pro Val		2064
	675	680	685
50	GTT CAG CTC CAT GGC TAC ATG GAA AAC AAG CCT CTG GGA CTT CAG ATC Val Gln Leu His Gly Tyr Met Glu Asn Lys Pro Leu Gly Leu Gln Ile		2112
	690	695	700
55	TTC ATT GGG ACA GCT GAT GAG CGG ATC CTT AAG CCG CAC GCC TTC TAC Phe Ile Gly Thr Ala Asp Glu Arg Ile Leu Lys Pro His Ala Phe Tyr		2160
	705	710	715
	CAG GTG CAC CGA ATC ACG GGG AAA ACT GTC ACC ACC ACC AGC TAT GAG		2208

256

	Gln Val His Arg Ile Thr Gly Lys Thr Val Thr Thr Thr Ser Tyr Glu		
	725	730	735
5	AAG ATA GTG GGC AAC ACC AAA GTC CTG GAG ATC CCC TTG GAG CCC AAA Lys Ile Val Gly Asn Thr Lys Val Leu Glu Ile Pro Leu Glu Pro Lys		2256
	740	745	750
10	AAC AAC ATG AGG GCA ACC ATC GAC TGT GCG GGG ATC TTG AAG CTT AGA Asn Asn Met Arg Ala Thr Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg		2304
	755	760	765
	AAC GCC GAC ATT GAG CTG CGG AAA GGC GAG ACG GAC ATT GGA AGA AAG Asn Ala Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys		2352
	770	775	780
15	AAC ACG CGG GTG AGA CTG GTT TTC CGA GTT CAC ATC CCA GAG TCC AGT Asn Thr Arg Val Arg Leu Val Phe Arg Val His Ile Pro Glu Ser Ser		2400
	785	790	795
20	GGC AGA ATC GTC TCT TTA CAG ACT GCA TCT AAC CCC ATC GAG TGC TCC Gly Arg Ile Val Ser Leu Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser		2448
	805	810	815
25	CAG CGA TCT GCT CAC GAG CTG CCC ATG GTT GAA AGA CAA GAC ACA GAC Gln Arg Ser Ala His Glu Leu Pro Met Val Glu Arg Gln Asp Thr Asp		2496
	820	825	830
30	AGC TGC CTG GTC TAT GGC GGC CAG CAA ATG ATC CTC ACG GGG CAG AAC Ser Cys Leu Val Tyr Gly Gln Gln Met Ile Leu Thr Gly Gln Asn		2544
	835	840	845
	TTT ACA TCC GAG TCC AAA GTT GTG TTT ACT GAG AAG ACC ACA GAT GGA Phe Thr Ser Glu Ser Lys Val Val Phe Thr Glu Lys Thr Thr Asp Gly		2592
	850	855	860
35	CAG CAA ATT TGG GAG ATG GAA GCC ACG GTG GAT AAG GAC AAG AGC CAG Gln Gln Ile Trp Glu Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln		2640
	865	870	875
40	CCC AAC ATG CTT TTT GTT GAG ATC CCT GAA TAT CGG AAC AAG CAT ATC Pro Asn Met Leu Phe Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile		2688
	885	890	895
45	CGC ACA CCT GTA AAA GTG AAC TTC TAC GTC ATC AAT GGG AAG AGA AAA Arg Thr Pro Val Lys Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys		2736
	900	905	910
50	CGA AGT CAG CCT CAG CAC TTT ACC TAC CAC CCA GTC CCA GCC ATC AAG Arg Ser Gln Pro Gln His Phe Thr Tyr His Pro Val Pro Ala Ile Lys		2784
	915	920	925
	ACG GAG CCC ACG GAT GAA TAT GAC CCC ACT CTG ATC TGC AGC CCC ACC Thr Glu Pro Thr Asp Glu Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr		2832
	930	935	940
55	CAT GGA GGC CTG GGG AGC CAG CCT TAC TAC CCC CAG CAC CCG ATG GTG		2880

256

257

	His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val			
	945	950	955	960
5	GCC GAG TCC CCC TCC TGC CTC GTG GCC ACC ATG GCT CCC TGC CAG CAG			2928
	Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln			
	965	970	975	
10	TTC CGC ACG GGG CTC TCA TCC CCT GAC GCC CGC TAC CAG CAA CAG AAC			2976
	Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Asn			
	980	985	990	
15	CCA GCG GCC GTA CTC TAC CAG CGG AGC AAG AGC CTG AGC CCC AGC CTG			3024
	Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu			
	995	1000	1005	
20	CTG GGC TAT CAG CAG CCG GCC CTC ATG GCC GCC CCG CTG TCC CTT GCG			3072
	Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu Ala			
	1010	1015	1020	
25	GAC GCT CAC CGC TCT GTG CTG GTG CAC GCC GGC TCC CAG GGC CAG AGC			3120
	Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly Gln Ser			
	1025	1030	1035	1040
30	TCA GCC CTG CTC CAC CCC TCT CCG ACC AAC CAG CAG GGC TCG CCT GTG			3168
	Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala Ser Pro Val			
	1045	1050	1055	
35	ATC CAC TAC TCA CCC ACC AAC CAG CAG CTG CGC TGC GGA AGC CAC CAG			3216
	Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys Gly Ser His Gln			
	1060	1065	1070	
40	GAG TTC CAG CAC ATC ATG TAC TGC GAG AAT TTC GCA CCA GGC ACC ACC			3264
	Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr			
	1075	1080	1085	
45	AGA CCT GGC CCG CCC CCG GTC AGT CAA GGT CAG AGG CTG AGC CCG GGT			3312
	Arg Pro Gly Pro Pro Val Ser Gln Gly Gln Arg Leu Ser Pro Gly			
	1090	1095	1100	
50	TCC TAC CCC ACA GTC ATT CAG CAG CAG AAT GCC ACG AGC CAA AGA GCC			3360
	Ser Tyr Pro Thr Val Ile Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala			
	1105	1110	1115	1120
55	GCC AAA AAC GGA CCC CCG GTC AGT GAC CAA AAG GAA GTA TTA CCT GCG			3408
	Ala Lys Asn Gly Pro Pro Val Ser Asp Gln Lys Glu Val Leu Pro Ala			
	1125	1130	1135	
	GGG GTG ACC ATT AAA CAG GAG CAG AAC TTG GAC CAG ACC TAC TTG GAT			3456
	Gly Val Thr Ile Lys Gln Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp			
	1140	1145	1150	
	GAT GTT AAT GAA ATT ATC AGG AAG GAG TTT TCA GGA CCT CCT GCC AGA			3504
	Asp Val Asn Glu Ile Ile Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg			
	1155	1160	1165	
	AAT CAG ACG TAA			3516

257

Asn Gln Thr
1170

5 (2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 amino acids
- (B) TYPE: amino acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
30	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
35	130 135 140	
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
40	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
45	210 215 220	
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
	Gly Leu Arg Ser Arg Ala Met Asn Ala Pro Glu Arg Gln Pro Gln Pro	
	245 250 255	
50	Asp Gly Gly Asp Ala Pro Gly His Glu Pro Gly Gly Ser Pro Gln Asp	
	260 265 270	
	Glu Leu Asp Phe Ser Ile Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn	
	275 280 285	
	Glu Glu Glu Pro Asn Ala His Lys Val Ala Ser Pro Pro Ser Gly Pro	
55	290 295 300	
	Ala Tyr Pro Asp Asp Val Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro	

	305	310	315	320
	Leu Ala Ser Leu Ser Gly Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp			
	325	330	335	
5	Arg Val Gly Pro Gln Lys Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala			
	340	345	350	
	Ser Gly Leu Ser Pro Arg Ile Glu Ile Thr Pro Ser His Glu Leu Ile			
	355	360	365	
	Gln Ala Val Gly Pro Leu Arg Met Arg Asp Ala Gly Leu Leu Val Glu			
	370	375	380	
10	Gln Pro Pro Leu Ala Gly Val Ala Ala Ser Pro Arg Phe Thr Leu Pro			
	385	390	395	400
	Val Pro Gly Phe Glu Gly Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala			
	405	410	415	
15	Ser Ser Gly Ser Ser Ala Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr			
	420	425	430	
	Thr Ser Pro Cys Val Ser Pro Asn Asn Gly Gly Pro Asp Asp Leu Cys			
	435	440	445	
	Pro Gln Phe Gln Asn Ile Pro Ala His Tyr Ser Pro Arg Thr Ser Pro			
	450	455	460	
20	Ile Met Ser Pro Arg Thr Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg			
	465	470	475	480
	His Ser Pro Val Pro Arg Pro Ala Ser Arg Ser Ser Ser Pro Gly Ala			
	485	490	495	
	Lys Arg Arg His Ser Cys Ala Glu Ala Leu Val Ala Leu Pro Pro Gly			
25	500	505	510	
	Ala Ser Pro Gln Arg Ser Arg Ser Pro Ser Pro Gln Pro Ser Ser His			
	515	520	525	
	Val Ala Pro Gln Asp His Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala			
	530	535	540	
30	Gly Ser Ala Val Ile Met Asp Ala Leu Asn Ser Leu Ala Thr Asp Ser			
	545	550	555	560
	Pro Cys Gly Ile Pro Pro Lys Met Trp Lys Thr Ser Pro Asp Pro Ser			
	565	570	575	
	Pro Val Ser Ala Ala Pro Ser Lys Ala Gly Leu Pro Arg His Ile Tyr			
35	580	585	590	
	Pro Ala Val Glu Phe Leu Gly Pro Cys Glu Gln Gly Glu Arg Arg Asn			
	595	600	605	
	Ser Ala Pro Glu Ser Ile Leu Leu Val Pro Pro Thr Trp Pro Lys Pro			
	610	615	620	
40	Leu Val Pro Ala Ile Pro Ile Cys Ser Ile Pro Val Thr Ala Ser Leu			
	625	630	635	640
	Pro Pro Leu Glu Trp Pro Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu			
	645	650	655	
	Arg Ile Glu Val Gln Pro Lys Pro His His Arg Ala His Tyr Glu Thr			
45	660	665	670	
	Glu Gly Ser Arg Gly Ala Val Lys Ala Pro Thr Gly Gly His Pro Val			
	675	680	685	
	Val Gln Leu His Gly Tyr Met Glu Asn Lys Pro Leu Gly Leu Gln Ile			
	690	695	700	
50	Phe Ile Gly Thr Ala Asp Glu Arg Ile Leu Lys Pro His Ala Phe Tyr			
	705	710	715	720
	Gln Val His Arg Ile Thr Gly Lys Thr Val Thr Thr Ser Tyr Glu			
	725	730	735	
	Lys Ile Val Gly Asn Thr Lys Val Leu Glu Ile Pro Leu Glu Pro Lys			
55	740	745	750	
	Asn Asn Met Arg Ala Thr Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg			

260

	755	760	765
	Asn Ala Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys		
	770	775	780
5	Asn Thr Arg Val Arg Leu Val Phe Arg Val His Ile Pro Glu Ser Ser		
	785	790	795
	Gly Arg Ile Val Ser Leu Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser		800
	805	810	815
10	Gln Arg Ser Ala His Glu Leu Pro Met Val Glu Arg Gln Asp Thr Asp		
	820	825	830
	Ser Cys Leu Val Tyr Gly Gly Gln Gln Met Ile Leu Thr Gly Gln Asn		
	835	840	845
	Phe Thr Ser Glu Ser Lys Val Val Phe Thr Glu Lys Thr Thr Asp Gly		
	850	855	860
15	Gln Gln Ile Trp Glu Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln		
	865	870	875
	Pro Asn Met Leu Phe Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile		880
	885	890	895
	Arg Thr Pro Val Lys Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys		
	900	905	910
20	Arg Ser Gln Pro Gln His Phe Thr Tyr His Pro Val Pro Ala Ile Lys		
	915	920	925
	Thr Glu Pro Thr Asp Glu Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr		
	930	935	940
25	His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val		
	945	950	955
	Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln		960
	965	970	975
	Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Asn		
	980	985	990
30	Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu		
	995	1000	1005
	Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu Ala		
	1010	1015	1020
35	Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly Gln Ser		
	1025	1030	1035
	Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala Ser Pro Val		1040
	1045	1050	1055
	Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys Gly Ser His Gln		
	1060	1065	1070
40	Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr		
	1075	1080	1085
	Arg Pro Gly Pro Pro Pro Val Ser Gln Gly Gln Arg Leu Ser Pro Gly		
	1090	1095	1100
45	Ser Tyr Pro Thr Val Ile Gln Gln Asn Ala Thr Ser Gln Arg Ala		
	1095	1110	1115
	Ala Lys Asn Gly Pro Pro Val Ser Asp Gln Lys Glu Val Leu Pro Ala		1120
	1125	1130	1135
	Gly Val Thr Ile Lys Gln Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp		
	1140	1145	1150
50	Asp Val Asn Glu Ile Ile Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg		
	1155	1160	1165
	Asn Gln Thr		
	1170		

55 (2) INFORMATION FOR SEQ ID NO:132:

261

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 3546 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(ix) FEATURE:	
10	(A) NAME/KEY: Coding Sequence	
	(B) LOCATION: 1...3543	
	(D) OTHER INFORMATION:	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
	ATG AAC GCC CCC GAG CGG CAG CCC CAA CCC GAC GGC GGG GAC GCC CCA	48
	Met Asn Ala Pro Glu Arg Gln Pro Gln Pro Asp Gly Gly Asp Ala Pro	
	1 5 10 15	
20	GGC CAC GAG CCT GGG GGC AGC CCC CAA GAC GAG CTT GAC TTC TCC ATC	96
	Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile	
	20 25 30	
25	CTC TTC GAC TAT GAG TAT TTG AAT CCG AAC GAA GAA GAG CCG AAT GCA	144
	Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala	
	35 40 45	
30	CAT AAG GTC GCC AGC CCA CCC TCC GGA CCC GCA TAC CCC GAT GAT GTA	192
	His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val	
	50 55 60	
35	ATG GAC TAT GGC CTC AAG CCA TAC AGC CCC CTT GCT AGT CTC TCT GGC	240
	Met Asp Tyr Glu Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly	
	65 70 75 80	
40	GAG CCC CCC GGC CGA TTC GGA GAG CCG GAT AGG GTA GGG CCG CAG AAG	288
	Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys	
	85 90 95	
45	TTT CTG AGC GCG GCC AAG CCA GCA GGG GCC TCG GGC CTG AGC CCT CGG	336
	Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala Ser Gly Leu Ser Pro Arg	
	100 105 110	
50	ATC GAG ATC ACT CCG TCC CAC GAA CTG ATC CAG GCA GTG GGG CCC CTC	384
	Ile Glu Ile Thr Pro Ser His Glu Leu Ile Gln Ala Val Gly Pro Leu	
	115 120 125	
55	CGC ATG AGA GAC GCG GGC CTC CTG GTG GAG CAG CCT CCC CTG GCC GGG	432
	Arg Met Arg Asp Ala Gly Leu Leu Val Glu Gln Pro Pro Leu Ala Gly	
	130 135 140	
	GTG GCC GCC AGC CCG AGG TTC ACC CTG CCC GTG CCC GGC TTC GAG GGC	480
	Val Ala Ala Ser Pro Arg Phe Thr Leu Pro Val Pro Gly Phe Glu Gly	
	145 150 155 160	
55	TAC CGC GAG CCG CTT TGC TTG AGC CCC GCT AGC AGC GGC TCC TCT GCC	528
	261	

262

	Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala Ser Ser Gly Ser Ser Ala		
	165	170	175
5	AGC TTC ATT TCT GAC ACC TTC TCC CCC TAC ACC TCG CCC TGC GTC TCG Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr Thr Ser Pro Cys Val Ser		576
	180	185	190
10	CCC AAT AAC GGC GGG CCC GAC GAC CTG TGT CCG CAG TTT CAA AAC ATC Pro Asn Asn Gly Gly Pro Asp Asp Leu Cys Pro Gln Phe Gln Asn Ile		624
	195	200	205
15	CCT GCT CAT TAT TCC CCC AGA ACC TCG CCA ATA ATG TCA CCT CGA ACC Pro Ala His Tyr Ser Pro Arg Thr Ser Pro Ile Met Ser Pro Arg Thr		672
	210	215	220
20	AGC CTC GCC GAG GAC AGC TGC CTG GGC CGC CAC TCG CCC GTG CCC CGT Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg His Ser Pro Val Pro Arg		720
	225	230	235
	240		
25	225	230	235
30	CCG GCC TCC CGC TCC TCA TCG CCT GGT GCC AAG CGG AGG CAT TCG TGC Pro Ala Ser Arg Ser Ser Pro Gly Ala Lys Arg Arg His Ser Cys		768
	245	250	255
35	GCC GAG GCC TTG GTT GCC CTG CCG CCC GGA GCC TCA CCC CAG CGC TCC Ala Glu Ala Leu Val Ala Leu Pro Pro Gly Ala Ser Pro Gln Arg Ser		816
	260	265	270
40	CGG AGC CCC TCG CCG CAG CCC TCA TCT CAC GTG GCA CCC CAG GAC CAC Arg Ser Pro Ser Pro Gln Pro Ser Ser His Val Ala Pro Gln Asp His		864
	275	280	285
45	275	280	285
50	GGC TCC CCG GCT GGG TAC CCC CCT GTG GCT GGC TCT GCC GTG ATC ATG Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala Gly Ser Ala Val Ile Met		912
	290	295	300
55	290	295	300
60	GAT GCC CTG AAC AGC CTC GCC ACG GAC TCG CCT TGT GGG ATC CCC CCC Asp Ala Leu Asn Ser Leu Ala Thr Asp Ser Pro Cys Gly Ile Pro Pro		960
	305	310	315
	320		
65	305	310	315
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1180	320		
1185	320		
1190	320		
1195	320		
1200	320		

263

	Ile Cys Ser Ile Pro Val Thr Ala Ser Leu Pro Pro Leu Glu Trp Pro		
385	390	395	400
5	CTG TCC AGT CAG TCA GGC TCT TAC GAG CTG CGG ATC GAG GTG CAG CCC Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu Arg Ile Glu Val Gln Pro		1248
	405	410	415
10	AAG CCA CAT CAC CGG GCC CAC TAT GAG ACA GAA GGC AGC CGA GGG GCT Lys Pro His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg Gly Ala		1296
	420	425	430
15	GTC AAA GCT CCA ACT GGA GGC CAC CCT GTG GTT CAG CTC CAT GGC TAC Val Lys Ala Pro Thr Gly Gly His Pro Val Val Gln Leu His Gly Tyr		1344
	435	440	445
20	ATG GAA AAC AAG CCT CTG GGA CTT CAG ATC TTC ATT GGG ACA GCT GAT Met Glu Asn Lys Pro Leu Gly Leu Gln Ile Phe Ile Gly Thr Ala Asp		1392
	450	455	460
25	GAG CGG ATC CTT AAG CCG CAC GCC TTC TAC CAG GTG CAC CGA ATC ACG Glu Arg Ile Leu Lys Pro His Ala Phe Tyr Gln Val His Arg Ile Thr		1440
	465	470	475
	485	490	495
30	GGG AAA ACT GTC ACC ACC ACC AGC TAT GAG AAG ATA GTG GGC AAC ACC Gly Lys Thr Val Thr Thr Ser Tyr Glu Lys Ile Val Gly Asn Thr		1488
	500	505	510
35	AAA GTC CTG GAG ATC CCC TTG GAG CCC AAA AAC AAC ATG AGG GCA ACC Lys Val Leu Glu Ile Pro Leu Glu Pro Lys Asn Asn Met Arg Ala Thr		1536
	515	520	525
40	ATC GAC TGT GCG GGG ATC TTG AAG CTT AGA AAC GCC GAC ATT GAG CTG Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ala Asp Ile Glu Leu		1584
	530	535	540
45	CGG AAA GGC GAG ACG GAC ATT GGA AGA AAG AAC ACG CGG GTG AGA CTG Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val Arg Leu		1632
	565	570	575
50	GTT TTC CGA GTT CAC ATC CCA GAG TCC AGT GGC AGA ATC GTC TCT TTA Val Phe Arg Val His Ile Pro Glu Ser Ser Gly Arg Ile Val Ser Leu		1680
	545	550	555
	580	585	590
55	CAG ACT GCA TCT AAC CCC ATC GAG TGC TCC CAG CGA TCT GCT CAC GAG Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala His Glu		1728
	595	600	605
	620	625	630
	640	645	650
	660	665	670
	680	685	690
	700	705	710
	720	725	730
	740	745	750
	760	765	770
	780	785	790
	800	805	810
	820	825	830
	840	845	850
	860	865	870
	880	885	890
	900	905	910

264

	Val Val Phe Thr Glu Lys Thr Thr Asp Gly Gln Gln Ile Trp Glu Met		
610	615	620	
5	GAA GCC ACG GTG GAT AAG GAC AAG AGC CAG CCC AAC ATG CTT TTT GTT Glu Ala Thr Val Asp Lys Asp Lys Ser Gln Pro Asn Met Leu Phe Val		1920
625	630	635	640
10	GAG ATC CCT GAA TAT CGG AAC AAG CAT ATC CGC ACA CCT GTA AAA GTG Glu Ile Pro Glu Tyr Arg Asn Lys His Ile Arg Thr Pro Val Lys Val		1968
645	650	655	
15	AAC TTC TAC GTC ATC AAT GGG AAG AGA AAA CGA AGT CAG CCT CAG CAC Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys Arg Ser Gln Pro Gln His		2016
660	665	670	
20	TTT ACC TAC CAC CCA GTC CCA GCC ATC AAG ACG GAG CCC ACG GAT GAA Phe Thr Tyr His Pro Val Pro Ala Ile Lys Thr Glu Pro Thr Asp Glu		2064
675	680	685	
25	TAT GAC CCC ACT CTG ATC TGC AGC CCC ACC CAT GGA GGC CTG GGG AGC Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr His Gly Gly Leu Gly Ser		2112
690	695	700	
30	CAG CCT TAC TAC CCC CAG CAC CCG ATG GTG GCC GAG TCC CCC TCC TGC Gln Pro Tyr Tyr Pro Gln His Pro Met Val Ala Glu Ser Pro Ser Cys		2160
705	710	715	720
35	CTC GTG GCC ACC ATG GCT CCC TGC CAG CAG TTC CGC ACG GGG CTC TCA Leu Val Ala Thr Met Ala Pro Cys Gln Gln Phe Arg Thr Gly Leu Ser		2208
725	730	735	
40	TCC CCT GAC GCC CGC TAC CAG CAA CAG AAC CCA GCG GCC GTA CTC TAC Ser Pro Asp Ala Arg Tyr Gln Gln Asn Pro Ala Ala Val Leu Tyr		2256
740	745	750	
45	CAG CGG AGC AAG AGC CTG AGC CCC AGC CTG CTG GGC TAT CAG CAG CCG Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu Leu Gly Tyr Gln Gln Pro		2304
755	760	765	
50	GCC CTC ATG GCC CGC CTG TCC CTT GCG GAC GCT CAC CGC TCT GTG Ala Leu Met Ala Ala Pro Leu Ser Leu Ala Asp Ala His Arg Ser Val		2352
770	775	780	
55	CTG GTG CAC GCC GGC TCC CAG GGC CAG AGC TCA GCC CTG CTC CAC CCC Leu Val His Ala Gly Ser Gln Gly Gln Ser Ser Ala Leu Leu His Pro		2400
785	790	795	800
55	TCT CCG ACC AAC CAG CAG GCC TCG CCT GTG ATC CAC TAC TCA CCC ACC Ser Pro Thr Asn Gln Gln Ala Ser Pro Val Ile His Tyr Ser Pro Thr		2448
805	810	815	
55	AAC CAG CAG CTG CGC TGC GGA AGC CAC CAG GAG TTC CAG CAC ATC ATG Asn Gln Gln Leu Arg Cys Gly Ser His Gln Glu Phe Gln His Ile Met		2496
820	825	830	
55	TAC TGC GAG AAT TTC GCA CCA GGC ACC ACC AGA CCT GGC CCG CCC CCG		2544
			264

265

	Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr Arg Pro Gly Pro Pro Pro			
	835	840	845	
5	GTC AGT CAA GGT CAG AGG CTG AGC CCG GGT TCC TAC CCC ACA GTC ATT Val Ser Gln Gln Gly Gln Arg Leu Ser Pro Gly Ser Tyr Pro Thr Val Ile			2592
	850	855	860	
10	CAG CAG CAG AAT GCC ACG AGC CAA AGA GCC GCC AAA AAC GGA CCC CCG Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala Ala Lys Asn Gly Pro Pro			2640
	865	870	875	880
	GTC AGT GAC CAA AAG GAA GTA TTA CCT GCG GGG GTG ACC ATT AAA CAG Val Ser Asp Gln Lys Glu Val Leu Pro Ala Gly Val Thr Ile Lys Gln			2688
	885	890	895	
15	GAG CAG AAC TTG GAC CAG ACC TAC TTG GAT GAT GTT AAT GAA ATT ATC Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp Asp Val Asn Glu Ile Ile			2736
	900	905	910	
20	AGG AAG GAG TTT TCA GGA CCT CCT GCC AGA AAT CAG ACG AGA ATT CTG Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg Asn Gln Thr Arg Ile Leu			2784
	915	920	925	
25	CAG TCG ACG GTA CCG CGG GCC CGG GAT CCA CCG GTC GCC ACC ATG GTG Gln Ser Thr Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met Val			2832
	930	935	940	
30	AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu			2880
	945	950	955	960
	CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly			2928
	965	970	975	
35	GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr			2976
	980	985	990	
40	ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr			3024
	995	1000	1005	
45	TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His			3072
	1010	1015	1020	
50	GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr			3120
	1025	1030	1035	1040
	ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			3168
	1045	1050	1055	
55	TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC			3216
	265			

266

	Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp		
	1060	1065	1070
5	TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC		3264
	Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr		
	1075	1080	1085
10	AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC		3312
	Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile		
	1090	1095	1100
	AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG		3360
	Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln		
	1105	1110	1115
15	CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG		3408
	Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val		
	1125	1130	1135
20	CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA		3456
	Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys		
	1140	1145	1150
25	GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC		3504
	Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr		
	1155	1160	1165
30	GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA		3546
	Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:133:

35	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 1181 amino acids		
	(B) TYPE: amino acid		
	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
40	(ii) MOLECULE TYPE: protein		
	(v) FRAGMENT TYPE: internal		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:		
	Met Asn Ala Pro Glu Arg Gln Pro Gln Pro Asp Gly Gly Asp Ala Pro		
	1 5 10 15		
	Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile		
	20 25 30		
50	Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Pro Asn Ala		
	35 40 45		
	His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val		
	50 55 60		
	Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly		
	65 70 75 80		
55	Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys		

266

267

	85	90	95
	Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala Ser Gly Leu Ser Pro Arg		
	100	105	110
5	Ile Glu Ile Thr Pro Ser His Glu Leu Ile Gln Ala Val Gly Pro Leu		
	115	120	125
	Arg Met Arg Asp Ala Gly Leu Leu Val Glu Gln Pro Pro Leu Ala Gly		
	130	135	140
	Val Ala Ala Ser Pro Arg Phe Thr Leu Pro Val Pro Gly Phe Gly		
	145	150	155
10	Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala Ser Ser Gly Ser Ser Ala		
	165	170	175
	Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr Thr Ser Pro Cys Val Ser		
	180	185	190
	Pro Asn Asn Gly Gly Pro Asp Asp Leu Cys Pro Gln Phe Gln Asn Ile		
15	195	200	205
	Pro Ala His Tyr Ser Pro Arg Thr Ser Pro Ile Met Ser Pro Arg Thr		
	210	215	220
	Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg His Ser Pro Val Pro Arg		
	225	230	235
20	Pro Ala Ser Arg Ser Ser Ser Pro Gly Ala Lys Arg Arg His Ser Cys		
	245	250	255
	Ala Glu Ala Leu Val Ala Leu Pro Pro Gly Ala Ser Pro Gln Arg Ser		
	260	265	270
25	Arg Ser Pro Ser Pro Gln Pro Ser Ser His Val Ala Pro Gln Asp His		
	275	280	285
	Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala Gly Ser Ala Val Ile Met		
	290	295	300
	Asp Ala Leu Asn Ser Leu Ala Thr Asp Ser Pro Cys Gly Ile Pro Pro		
	305	310	315
30	Lys Met Trp Lys Thr Ser Pro Asp Pro Ser Pro Val Ser Ala Ala Pro		
	325	330	335
	Ser Lys Ala Gly Leu Pro Arg His Ile Tyr Pro Ala Val Glu Phe Leu		
	340	345	350
	Gly Pro Cys Glu Gln Gly Glu Arg Arg Asn Ser Ala Pro Glu Ser Ile		
35	355	360	365
	Leu Leu Val Pro Pro Thr Trp Pro Lys Pro Leu Val Pro Ala Ile Pro		
	370	375	380
	Ile Cys Ser Ile Pro Val Thr Ala Ser Leu Pro Pro Leu Glu Trp Pro		
	385	390	395
40	Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu Arg Ile Glu Val Gln Pro		
	405	410	415
	Lys Pro His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg Gly Ala		
	420	425	430
	Val Lys Ala Pro Thr Gly Gly His Pro Val Val Gln Leu His Gly Tyr		
45	435	440	445
	Met Glu Asn Lys Pro Leu Gly Leu Gln Ile Phe Ile Gly Thr Ala Asp		
	450	455	460
	Glu Arg Ile Leu Lys Pro His Ala Phe Tyr Gln Val His Arg Ile Thr		
	465	470	475
50	Gly Lys Thr Val Thr Thr Ser Tyr Glu Lys Ile Val Gly Asn Thr		
	485	490	495
	Lys Val Leu Glu Ile Pro Leu Glu Pro Lys Asn Asn Met Arg Ala Thr		
	500	505	510
	Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ala Asp Ile Glu Leu		
55	515	520	525
	Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val Arg Leu		

268

	530	535	540
	Val Phe Arg Val His Ile Pro Glu Ser Ser Gly Arg Ile Val Ser Leu		
545	550	555	560
	Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala His Glu		
5	565	570	575
	Leu Pro Met Val Glu Arg Gln Asp Thr Asp Ser Cys Leu Val Tyr Gly		
	580	585	590
	Gly Gln Gln Met Ile Leu Thr Gly Gln Asn Phe Thr Ser Glu Ser Lys		
	595	600	605
10	Val Val Phe Thr Glu Lys Thr Thr Asp Gly Gln Gln Ile Trp Glu Met		
	610	615	620
	Glu Ala Thr Val Asp Lys Asp Lys Ser Gln Pro Asn Met Leu Phe Val		
625	630	635	640
	Glu Ile Pro Glu Tyr Arg Asn Lys His Ile Arg Thr Pro Val Lys Val		
15	645	650	655
	Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys Arg Ser Gln Pro Gln His		
	660	665	670
	Phe Thr Tyr His Pro Val Pro Ala Ile Lys Thr Glu Pro Thr Asp Glu		
	675	680	685
20	Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr His Gly Gly Leu Gly Ser		
	690	695	700
	Gln Pro Tyr Tyr Pro Gln His Pro Met Val Ala Glu Ser Pro Ser Cys		
705	710	715	720
	Leu Val Ala Thr Met Ala Pro Cys Gln Gln Phe Arg Thr Gly Leu Ser		
25	725	730	735
	Ser Pro Asp Ala Arg Tyr Gln Gln Asn Pro Ala Ala Val Leu Tyr		
	740	745	750
	Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu Leu Gly Tyr Gln Gln Pro		
	755	760	765
30	Ala Leu Met Ala Ala Pro Leu Ser Leu Ala Asp Ala His Arg Ser Val		
	770	775	780
	Leu Val His Ala Gly Ser Gln Gly Gln Ser Ser Ala Leu Leu His Pro		
785	790	795	800
	Ser Pro Thr Asn Gln Gln Ala Ser Pro Val Ile His Tyr Ser Pro Thr		
35	805	810	815
	Asn Gln Gln Leu Arg Cys Gly Ser His Gln Glu Phe Gln His Ile Met		
	820	825	830
	Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr Arg Pro Gly Pro Pro Pro		
	835	840	845
40	Val Ser Gln Gly Gln Arg Leu Ser Pro Gly Ser Tyr Pro Thr Val Ile		
	850	855	860
	Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala Ala Lys Asn Gly Pro Pro		
865	870	875	880
	Val Ser Asp Gln Lys Glu Val Leu Pro Ala Gly Val Thr Ile Lys Gln		
45	885	890	895
	Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp Asp Val Asn Glu Ile Ile		
	900	905	910
	Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg Asn Gln Thr Arg Ile Leu		
	915	920	925
50	Gln Ser Thr Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met Val		
	930	935	940
	Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu		
945	950	955	960
	Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly		
55	965	970	975
	Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr		

269

	980	985	990
	Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr		
	995	1000	1005
5	Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His		
	1010	1015	1020
	Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr		
	025	1030	1035
10	Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys		
	1045	1050	1055
	Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp		
	1060	1065	1070
	Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr		
	1075	1080	1085
15	Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile		
	1090	1095	1100
	Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln		
	1095	1110	1115
20	Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val		
	1125	1130	1135
	Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys		
	1140	1145	1150
	Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr		
	1155	1160	1165
25	Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2802 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2799
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

45	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
50	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
55	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192

270

	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
	50	55	60
5	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		240
	65	70	75
	80		
10	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		288
	85	90	95
15	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		336
	100	105	110
20	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		384
	115	120	125
25	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		432
	130	135	140
30	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		480
	145	150	155
	160		
35	GAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		528
	165	170	175
40	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		576
	180	185	190
45	195	200	205
50	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		624
	210	215	220
55	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		672
	225	230	235
	240		
50	GGA CTC AGA TCT CGA GGG AGC ATG GGC ACC TTG CGG GAT TTA CAG TAC Gly Leu Arg Ser Arg Gly Ser Met Gly Thr Leu Arg Asp Leu Gln Tyr		720
	245	250	255
55	GCG CTC CAG GAG AAG ATC GAG GAG CTG AGG CAG CGG GAT GCT CTC ATC Ala Leu Gln Glu Lys Ile Glu Glu Leu Arg Gln Arg Asp Ala Leu Ile		768
	260	265	270
55	GAC GAG CTG GAG CTG GAG TTG GAT CAG AAG GAC GAA CTG ATC CAG AAG		816
	864		

270

271

	Asp Glu Leu Glu Leu Glu Leu Asp Gln Lys Asp Glu Leu Ile Gln Lys		
	275	280	285
5	CTG CAG AAC GAG CTG GAC AAG TAC CGC TCG GTG ATC CGA CCA GCC ACC Leu Gln Asn Glu Leu Asp Lys Tyr Arg Ser Val Ile Arg Pro Ala Thr		912
	290	295	300
10	CAG CAG GCG CAG AAG CAG AGC GCG AGC ACC TTG CAG GGC GAG CCG CGC Gln Gln Ala Gln Lys Gln Ser Ala Ser Thr Leu Gln Gly Glu Pro Arg		960
	305	310	315
	320		
	ACC AAG CGG CAG GCG ATC TCC GCC GAG CCC ACC GCC TTC GAC ATC CAG Thr Lys Arg Gln Ala Ile Ser Ala Glu Pro Thr Ala Phe Asp Ile Gln		1008
	325	330	335
15	GAT CTC AGC CAT GTG ACC CTG CCC TTC TAC CCC AAG AGC CCA CAG TCC Asp Leu Ser His Val Thr Leu Pro Phe Tyr Pro Lys Ser Pro Gln Ser		1056
	340	345	350
20	AAG GAT CTT ATA AAG GAA GCT ATC CTT GAC AAT GAC TTT ATG AAG AAC Lys Asp Leu Ile Lys Glu Ala Ile Leu Asp Asn Asp Phe Met Lys Asn		1104
	355	360	365
25	TTG GAG CTG TCG CAG ATC CAG GAG ATT GTG GAT TGT ATG TAC CCG GTG Leu Glu Leu Ser Gln Ile Gln Glu Ile Val Asp Cys Met Tyr Pro Val		1152
	370	375	380
30	GAG TAT GGC AAG GAC AGT TGC ATC ATC AAA GAA GGA GAC GTG GGG TCA Glu Tyr Gly Lys Asp Ser Cys Ile Ile Lys Glu Gly Asp Val Gly Ser		1200
	385	390	395
	400		
	CTG GTG TAT GTC ATG GAA GAT GGT AAG GTT GAA GTT ACA AAA GAA GGT Leu Val Tyr Val Met Glu Asp Gly Lys Val Glu Val Thr Lys Glu Gly		1248
	405	410	415
35	GTG AAG TTG TGT ACC ATG GGT CCA GGA AAA GTG TTT GGG GAA TTG GCT Val Lys Leu Cys Thr Met Gly Pro Gly Lys Val Phe Gly Glu Leu Ala		1296
	420	425	430
40	ATT CTT TAC AAC TGT ACC CGG ACA GCG ACC GTC AAG ACT CTT GTA AAT Ile Leu Tyr Asn Cys Thr Arg Thr Ala Thr Val Lys Thr Leu Val Asn		1344
	435	440	445
45	GTA AAA CTC TGG GCC ATT GAT CGA CAA TGT TTT CAA ACA ATA ATG ATG Val Lys Leu Trp Ala Ile Asp Arg Gln Cys Phe Gln Thr Ile Met Met		1392
	450	455	460
50	AGG ACA GGA CTC ATC AAG CAT ACC GAG TAT ATG GAA TTT TTA AAA AGC Arg Thr Gly Leu Ile Lys His Thr Glu Tyr Met Glu Phe Leu Lys Ser		1440
	465	470	475
	480		
	GTT CCA ACA TTC CAG AGC CTT CCT GAA GAG ATC CTC AGC AAG CTT GCT Val Pro Thr Phe Gln Ser Leu Pro Glu Glu Ile Leu Ser Lys Leu Ala		1488
	485	490	495
55	GAT GTC CTT GAA GAG ACC CAC TAT GAA AAT GGA GAA TAT ATT ATC AGG		1536

272

	Asp Val Leu Glu Glu Thr His Tyr Glu Asn Gly Glu Tyr Ile Ile Arg		
	500	505	510
5	CAA GGT GCA AGA GGG GAC ACC TTC TTT ATC ATC AGC AAA GGA ACG GTA Gln Gly Ala Arg Gly Asp Thr Phe Phe Ile Ile Ser Lys Gly Thr Val	515	520
	525		
10	AAT GTC ACT CGT GAA GAC TCA CCG AGT GAA GAC CCA GTC TTT CTT AGA Asn Val Thr Arg Glu Asp Ser Pro Ser Glu Asp Pro Val Phe Leu Arg	530	535
	540		
15	ACT TTA GGA AAA GGA GAC TGG TTT GGA GAG AAA GCC TTG CAG GGG GAA Thr Leu Gly Lys Gly Asp Trp Phe Gly Glu Lys Ala Leu Gln Gly Glu	545	550
	555	560	
20	GAT GTG AGA ACA GCA AAC GTA ATT GCT GCA GAA GCT GTA ACC TGC CTT Asp Val Arg Thr Ala Asn Val Ile Ala Ala Glu Ala Val Thr Cys Leu	565	570
	575		
25	GTG ATT GAC AGA GAC TCT TTT AAA CAT TTG ATT GGA GGG CTG GAT GAT Val Ile Asp Arg Asp Ser Phe Lys His Leu Ile Gly Gly Leu Asp Asp	580	585
	590		
30	GTT TCT AAT AAA GCA TAT GAA GAT GCA GAA GCT AAA GCA AAA TAT GAA Val Ser Asn Lys Ala Tyr Glu Asp Ala Glu Ala Lys Ala Lys Tyr Glu	595	600
	605		
35	GCT GAA GCG GCT TTC GCC AAC CTG AAG CTG TCT GAT TTC AAC ATC Ala Glu Ala Ala Phe Phe Ala Asn Leu Lys Leu Ser Asp Phe Asn Ile	610	615
	620		
40	ATT GAT ACC CTT GGA GTT GGA GGT TTC GGA CGA GTA GAA CTG GTC CAG Ile Asp Thr Leu Gly Val Gly Phe Gly Arg Val Glu Leu Val Gln	625	630
	635	640	
45	TTG AAA AGT GAA GAA TCC AAA ACG TTT GCA ATG AAG ATT CTC AAG AAA Leu Lys Ser Glu Glu Ser Lys Thr Phe Ala Met Lys Ile Leu Lys Lys	645	650
	655		
50	CGT CAC ATT GTG GAC ACA AGA CAG CAG GAG CAC ATC CGC TCA GAG AAG Arg His Ile Val Asp Thr Arg Gln Gln Glu His Ile Arg Ser Glu Lys	660	665
	670		
55	CAG ATC ATG CAG GGG GCT CAT TCC GAT TTC ATA GTG AGA CTG TAC AGA Gln Ile Met Gln Gly Ala His Ser Asp Phe Ile Val Arg Leu Tyr Arg	675	680
	685		
60	ACA TTT AAG GAC AGC AAA TAT TTG TAT ATG TTG ATG GAA GCT TGT CTA Thr Phe Lys Asp Ser Lys Tyr Leu Tyr Met Leu Met Glu Ala Cys Leu	690	695
	700		
65	GGT GGA GAG CTC TGG ACC ATT CTC AGG GAT AGA GGT TCG TTT GAA GAT Gly Gly Glu Leu Trp Thr Ile Leu Arg Asp Arg Gly Ser Phe Glu Asp	705	710
	715	720	
70	TCT ACA ACC AGA TTT TAC ACA GCA TGT GTG GTA GAA GCT TTT GCC TAT		
			2208

272

273

	Ser Thr Thr Arg Phe Tyr Thr Ala Cys Val Val Glu Ala Phe Ala Tyr		
	725	730	735
5	CTG CAT TCC AAA GGA ATC ATT TAC AGG GAC CTC AAG CCA GAA AAT CTC Leu His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu		2256
	740	745	750
10	ATC CTA GAT CAC CGA GGT TAT GCC AAA CTG GTT GAT TTT GGC TTT GCA Ile Leu Asp His Arg Gly Tyr Ala Lys Leu Val Asp Phe Gly Phe Ala		2304
	755	760	765
	AAG AAA ATA GGA TTT GGA AAG AAA ACA TGG ACT TTT TGT GGG ACT CCA Lys Lys Ile Gly Phe Gly Lys Lys Thr Trp Thr Phe Cys Gly Thr Pro		2352
15	770	775	780
	GAG TAT GTA GCC CCA GAG ATC ATC CTG AAC AAA GGC CAT GAC ATT TCA Glu Tyr Val Ala Pro Glu Ile Ile Leu Asn Lys Gly His Asp Ile Ser		2400
	785	790	795
20	GCC GAC TAC TGG TCA CTG GGA ATC CTA ATG TAT GAA CTC CTG ACT GGC Ala Asp Tyr Trp Ser Leu Gly Ile Leu Met Tyr Glu Leu Leu Thr Gly		2448
	805	810	815
25	AGC CCA CCT TTC TCA GGC CCA GAT CCT ATG AAA ACC TAT AAC ATC ATA Ser Pro Pro Phe Ser Gly Pro Asp Pro Met Lys Thr Tyr Asn Ile Ile		2496
	820	825	830
30	TTG AGG GGG ATT GAC ATG ATA GAA TTT CCA AAG AAG ATT GCC AAA AAT Leu Arg Gly Ile Asp Met Ile Glu Phe Pro Lys Lys Ile Ala Lys Asn		2544
	835	840	845
	GCT GCT AAT TTA ATT AAA AAA CTA TGC AGG GAC AAT CCA TCA GAA AGA Ala Ala Asn Leu Ile Lys Lys Leu Cys Arg Asp Asn Pro Ser Glu Arg		2592
35	850	855	860
	TTA GGG AAT TTG AAA AAT GGA GTA AAA GAC ATT CAA AAG CAC AAA TGG Leu Gly Asn Leu Lys Asn Gly Val Lys Asp Ile Gln Lys His Lys Trp		2640
	865	870	875
40	880	885	890
	TTT GAG GGC TTT AAC TGG GAA GGC TTA AGA AAA GGT ACC TTG ACA CCT Phe Glu Gly Phe Asn Trp Glu Gly Leu Arg Lys Gly Thr Leu Thr Pro		2688
	895		
45	CCT ATA ATA CCA AGT GTT GCA TCA CCC ACA GAC ACA AGT AAT TTT GAC Pro Ile Ile Pro Ser Val Ala Ser Pro Thr Asp Thr Ser Asn Phe Asp		2736
	900	905	910
	AGT TTC CCT GAG GAC AAC GAT GAA CCA CCA CCT GAT GAC AAC TCA GGA Ser Phe Pro Glu Asp Asn Asp Glu Pro Pro Pro Asp Asp Asn Ser Gly		2784
50	915	920	925
	TGG GAT ATA GAC TTC TAA Trp Asp Ile Asp Phe 930		2802

55

273

274

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 933 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

15	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
	1	5	10	15
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
	20	25	30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	35	40	45	
20	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
	50	55	60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
	65	70	75	80
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
25	85	90	95	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
	100	105	110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
	115	120	125	
30	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
	130	135	140	
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
	145	150	155	160
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
35	165	170	175	
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
	180	185	190	
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
	195	200	205	
40	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
	210	215	220	
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
	225	230	235	240
	Gly Leu Arg Ser Arg Gly Ser Met Gly Thr Leu Arg Asp Leu Gln Tyr			
45	245	250	255	
	Ala Leu Gln Glu Lys Ile Glu Glu Leu Arg Gln Arg Asp Ala Leu Ile			
	260	265	270	
	Asp Glu Leu Glu Leu Glu Leu Asp Gln Lys Asp Glu Leu Ile Gln Lys			
	275	280	285	
50	Leu Gln Asn Glu Leu Asp Lys Tyr Arg Ser Val Ile Arg Pro Ala Thr			
	290	295	300	
	Gln Gln Ala Gln Lys Gln Ser Ala Ser Thr Leu Gln Gly Glu Pro Arg			
	305	310	315	320
	Thr Lys Arg Gln Ala Ile Ser Ala Glu Pro Thr Ala Phe Asp Ile Gln			
55	325	330	335	
	Asp Leu Ser His Val Thr Leu Pro Phe Tyr Pro Lys Ser Pro Gln Ser			

275

	340	345	350
	Lys Asp Leu Ile Lys Glu Ala Ile Leu Asp Asn Asp Phe Met Lys Asn		
	355	360	365
5	Leu Glu Leu Ser Gln Ile Gln Glu Ile Val Asp Cys Met Tyr Pro Val		
	370	375	380
	Glu Tyr Gly Lys Asp Ser Cys Ile Ile Lys Glu Gly Asp Val Gly Ser		
	385	390	395
	400		
	Leu Val Tyr Val Met Glu Asp Gly Lys Val Glu Val Thr Lys Glu Gly		
	405	410	415
10	Val Lys Leu Cys Thr Met Gly Pro Gly Lys Val Phe Gly Glu Leu Ala		
	420	425	430
	Ile Leu Tyr Asn Cys Thr Arg Thr Ala Thr Val Lys Thr Leu Val Asn		
	435	440	445
15	Val Lys Leu Trp Ala Ile Asp Arg Gln Cys Phe Gln Thr Ile Met Met		
	450	455	460
	Arg Thr Gly Leu Ile Lys His Thr Glu Tyr Met Glu Phe Leu Lys Ser		
	465	470	475
	480		
	Val Pro Thr Phe Gln Ser Leu Pro Glu Glu Ile Leu Ser Lys Leu Ala		
	485	490	495
20	Asp Val Leu Glu Glu Thr His Tyr Glu Asn Gly Glu Tyr Ile Ile Arg		
	500	505	510
	Gln Gly Ala Arg Gly Asp Thr Phe Phe Ile Ile Ser Lys Gly Thr Val		
	515	520	525
25	Asn Val Thr Arg Glu Asp Ser Pro Ser Glu Asp Pro Val Phe Leu Arg		
	530	535	540
	Thr Leu Gly Lys Gly Asp Trp Phe Gly Glu Lys Ala Leu Gln Gly Glu		
	545	550	555
	560		
	Asp Val Arg Thr Ala Asn Val Ile Ala Ala Glu Ala Val Thr Cys Leu		
	565	570	575
30	Val Ile Asp Arg Asp Ser Phe Lys His Leu Ile Gly Gly Leu Asp Asp		
	580	585	590
	Val Ser Asn Lys Ala Tyr Glu Asp Ala Glu Ala Lys Ala Lys Tyr Glu		
	595	600	605
35	Ala Glu Ala Ala Phe Phe Ala Asn Leu Lys Leu Ser Asp Phe Asn Ile		
	610	615	620
	Ile Asp Thr Leu Gly Val Gly Gly Phe Gly Arg Val Glu Leu Val Gln		
	625	630	635
	640		
	Leu Lys Ser Glu Glu Ser Lys Thr Phe Ala Met Lys Ile Leu Lys Lys		
	645	650	655
40	Arg His Ile Val Asp Thr Arg Gln Gln Glu His Ile Arg Ser Glu Lys		
	660	665	670
	Gln Ile Met Gln Gly Ala His Ser Asp Phe Ile Val Arg Leu Tyr Arg		
	675	680	685
45	Thr Phe Lys Asp Ser Lys Tyr Leu Tyr Met Leu Met Glu Ala Cys Leu		
	690	695	700
	Gly Gly Glu Leu Trp Thr Ile Leu Arg Asp Arg Gly Ser Phe Glu Asp		
	705	710	715
	720		
	Ser Thr Thr Arg Phe Tyr Thr Ala Cys Val Val Glu Ala Phe Ala Tyr		
	725	730	735
50	Leu His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu		
	740	745	750
	Ile Leu Asp His Arg Gly Tyr Ala Lys Leu Val Asp Phe Gly Phe Ala		
	755	760	765
55	Lys Lys Ile Gly Phe Gly Lys Lys Thr Trp Thr Phe Cys Gly Thr Pro		
	770	775	780
	Glu Tyr Val Ala Pro Glu Ile Ile Leu Asn Lys Gly His Asp Ile Ser		

276

	785	790	795	800
	Ala Asp Tyr Trp Ser Leu Gly Ile Leu Met		Tyr Glu Leu Leu Thr Gly	
	805		810	815
5	Ser Pro Pro Phe Ser Gly Pro Asp Pro	Met Lys Thr Tyr Asn Ile Ile		
	820	825	830	
	Leu Arg Gly Ile Asp Met Ile Glu Phe Pro Lys Lys Ile Ala Lys Asn			
	835	840	845	
10	Ala Ala Asn Leu Ile Lys Lys Leu Cys Arg Asp Asn Pro Ser Glu Arg			
	850	855	860	
15	Leu Gly Asn Leu Lys Asn Gly Val Lys Asp Ile Gln Lys His Lys Trp			
	865	870	875	880
	Phe Glu Gly Phe Asn Trp Glu Gly Leu Arg Lys Gly Thr Leu Thr Pro			
	885	890	895	
20	Pro Ile Ile Pro Ser Val Ala Ser Pro Thr Asp Thr Ser Asn Phe Asp			
	900	905	910	
	Ser Phe Pro Glu Asp Asn Asp Glu Pro Pro Pro Asp Asp Asn Ser Gly			
	915	920	925	
	Trp Asp Ile Asp Phe			
	930			

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...2795
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

	ATG GGC ACC TTG CGG GAT TTA CAG TAC GCG CTC CAG GAG AAG ATC GAG		48	
	Met Gly Thr Leu Arg Asp Leu Gln Tyr Ala Leu Gln Glu Lys Ile Glu			
40	1	5	10	15
	GAG CTG AGG CAG CGG GAT GCT CTC ATC GAC GAG CTG GAG CTG GAG TTG		96	
	Glu Leu Arg Gln Arg Asp Ala Leu Ile Asp Glu Leu Glu Leu Glu Leu			
	20	25	30	
45	GAT CAG AAG GAC GAA CTG ATC CAG AAG CTG CAG AAC GAG CTG GAC AAG		144	
	Asp Gln Lys Asp Glu Leu Ile Gln Lys Leu Gln Asn Glu Leu Asp Lys			
	35	40	45	
50	TAC CGC TCG GTG ATC CGA CCA GCC ACC CAG CAG GCG CAG AAG CAG AGC		192	
	Tyr Arg Ser Val Ile Arg Pro Ala Thr Gln Gln Ala Gln Lys Gln Ser			
	50	55	60	
55	GCG AGC ACC TTG CAG GGC GAG CCG CGC ACC AAG CGG CAG GCG ATC TCC		240	
	Ala Ser Thr Leu Gln Gly Glu Pro Arg Thr Lys Arg Gln Ala Ile Ser			
	65	70	75	80

276

	GCC GAG CCC ACC GCC TTC GAC ATC CAG GAT CTC AGC CAT GTG ACC CTG Ala Glu Pro Thr Ala Phe Asp Ile Gln Asp Leu Ser His Val Thr Leu 85 90 95	288
5	CCC TTC TAC CCC AAG AGC CCA CAG TCC AAG GAT CTT ATA AAG GAA GCT Pro Phe Tyr Pro Lys Ser Pro Gln Ser Lys Asp Leu Ile Lys Glu Ala 100 105 110	336
10	ATC CTT GAC AAT GAC TTT ATG AAG AAC TTG GAG CTG TCG CAG ATC CAG Ile Leu Asp Asn Asp Phe Met Lys Asn Leu Glu Leu Ser Gln Ile Gln 115 120 125	384
15	GAG ATT GTG GAT TGT ATG TAC CCG GTG GAG TAT GGC AAG GAC AGT TGC Glu Ile Val Asp Cys Met Tyr Pro Val Glu Tyr Gly Lys Asp Ser Cys 130 135 140	432
20	ATC ATC AAA GAA GGA GAC GTG GGG TCA CTG GTG TAT GTC ATG GAA GAT Ile Ile Lys Glu Gly Asp Val Gly Ser Leu Val Tyr Val Met Glu Asp 145 150 155 160	480
	GGT AAG GTT GAA GTT ACA AAA GAA GGT GTG AAG TTG TGT ACC ATG GGT Gly Lys Val Glu Val Thr Lys Glu Gly Val Lys Leu Cys Thr Met Gly 165 170 175	528
25	CCA GGA AAA GTG TTT GGG GAA TTG GCT ATT CTT TAC AAC TGT ACC CGG Pro Gly Lys Val Phe Gly Glu Leu Ala Ile Leu Tyr Asn Cys Thr Arg 180 185 190	576
30	ACA GCG ACC GTC AAG ACT CTT GTA AAT GTA AAA CTC TGG GCC ATT GAT Thr Ala Thr Val Lys Thr Leu Val Asn Val Lys Leu Trp Ala Ile Asp 195 200 205	624
35	CGA CAA TGT TTT CAA ACA ATA ATG ATG AGG ACA GGA CTC ATC AAG CAT Arg Gln Cys Phe Gln Thr Ile Met Met Arg Thr Gly Leu Ile Lys His 210 215 220	672
40	ACC GAG TAT ATG GAA TTT TTA AAA AGC GTT CCA ACA TTC CAG AGC CTT Thr Glu Tyr Met Glu Phe Leu Lys Ser Val Pro Thr Phe Gln Ser Leu 225 230 235 240	720
	CCT GAA GAG ATC CTC AGC AAG CTT GCT GAT GTC CTT GAA GAG ACC CAC Pro Glu Glu Ile Leu Ser Lys Leu Ala Asp Val Leu Glu Glu Thr His 245 250 255	768
45	TAT GAA AAT GGA GAA TAT ATT ATC AGG CAA GGT GCA AGA GGG GAC ACC Tyr Glu Asn Gly Glu Tyr Ile Ile Arg Gln Gly Ala Arg Gly Asp Thr 260 265 270	816
50	TTC TTT ATC ATC AGC AAA GGA ACG GTA AAT GTC ACT CGT GAA GAC TCA Phe Phe Ile Ile Ser Lys Gly Thr Val Asn Val Thr Arg Glu Asp Ser 275 280 285	864
55	CCG AGT GAA GAC CCA GTC TTT CTT AGA ACT TTA GGA AAA GGA GAC TGG Pro Ser Glu Asp Pro Val Phe Leu Arg Thr Leu Gly Lys Gly Asp Trp 290 295 300	912

	TTT GGA GAG AAA GCC TTG CAG GGG GAA GAT GTG AGA ACA GCA AAC GTA Phe Gly Glu Lys Ala Leu Gln Gly Glu Asp Val Arg Thr Ala Asn Val 305 310 315 320	960
5	ATT GCT GCA GAA GCT GTA ACC TGC CTT GTG ATT GAC AGA GAC TCT TTT Ile Ala Ala Glu Ala Val Thr Cys Leu Val Ile Asp Arg Asp Ser Phe 325 330 335	1008
10	AAA CAT TTG ATT GGA GGG CTG GAT GAT GTT TCT AAT AAA GCA TAT GAA Lys His Leu Ile Gly Gly Leu Asp Asp Val Ser Asn Lys Ala Tyr Glu 340 345 350	1056
15	GAT GCA GAA GCT AAA GCA AAA TAT GAA GCT GAA GCG GCT TTC TTC GCC Asp Ala Glu Ala Lys Ala Lys Tyr Glu Ala Glu Ala Ala Phe Phe Ala 355 360 365	1104
20	AAC CTG AAG CTG TCT GAT TTC AAC ATC ATT GAT ACC CTT GGA GTT GGA Asn Leu Lys Leu Ser Asp Phe Asn Ile Ile Asp Thr Leu Gly Val Gly 370 375 380	1152
25	GGT TTC GGA CGA GTA GAA CTG GTC CAG TTG AAA AGT GAA GAA TCC AAA Gly Phe Gly Arg Val Glu Leu Val Gln Leu Lys Ser Glu Glu Ser Lys 385 390 395 400	1200
30	ACG TTT GCA ATG AAG ATT CTC AAG AAA CGT CAC ATT GTG GAC ACA AGA Thr Phe Ala Met Lys Ile Leu Lys Lys Arg His Ile Val Asp Thr Arg 405 410 415	1248
35	CAG CAG GAG CAC ATC CGC TCA GAG AAG CAG ATC ATG CAG GGG GCT CAT Gln Gln Glu His Ile Arg Ser Glu Lys Gln Ile Met Gln Gly Ala His 420 425 430	1296
40	TCC GAT TTC ATA GTG AGA CTG TAC AGA ACA TTT AAG GAC AGC AAA TAT Ser Asp Phe Ile Val Arg Leu Tyr Arg Thr Phe Lys Asp Ser Lys Tyr 435 440 445	1344
45	TTG TAT ATG TTG ATG GAA GCT TGT CTA GGT GGA GAG CTC TGG ACC ATT Leu Tyr Met Leu Met Glu Ala Cys Leu Gly Gly Glu Leu Trp Thr Ile 450 455 460	1392
50	CTC AGG GAT AGA GGT TCG TTT GAA GAT TCT ACA ACC AGA TTT TAC ACA Leu Arg Asp Arg Gly Ser Phe Glu Asp Ser Thr Thr Arg Phe Tyr Thr 465 470 475 480	1440
55	GCA TGT GTG GTA GAA GCT TTT GCC TAT CTG CAT TCC AAA GGA ATC ATT Ala Cys Val Val Glu Ala Phe Ala Tyr Leu His Ser Lys Gly Ile Ile 485 490 495	1488
55	TAC AGG GAC CTC AAG CCA GAA AAT CTC ATC CTA GAT CAC CGA GGT TAT Tyr Arg Asp Leu Lys Pro Glu Asn Leu Ile Leu Asp His Arg Gly Tyr 500 505 510	1536
55	GCC AAA CTG GTT GAT TTT GGC TTT GCA AAG AAA ATA GGA TTT GGA AAG Ala Lys Leu Val Asp Phe Gly Phe Ala Lys Lys Ile Gly Phe Gly Lys 515 520 525	1584

	AAA ACA TGG ACT TTT TGT GGG ACT CCA GAG TAT GTA GCC CCA GAG ATC Lys Thr Trp Thr Phe Cys Gly Thr Pro Glu Tyr Val Ala Pro Glu Ile 530 535 540	1632
5	ATC CTG AAC AAA GGC CAT GAC ATT TCA GCC GAC TAC TGG TCA CTG GGA Ile Leu Asn Lys Gly His Asp Ile Ser Ala Asp Tyr Trp Ser Leu Gly 545 550 555 560	1680
10	ATC CTA ATG TAT GAA CTC CTG ACT GGC AGC CCA CCT TTC TCA GGC CCA Ile Leu Met Tyr Glu Leu Leu Thr Gly Ser Pro Pro Phe Ser Gly Pro 565 570 575	1728
15	GAT CCT ATG AAA ACC TAT AAC ATC ATA TTG AGG GGG ATT GAC ATG ATA Asp Pro Met Lys Thr Tyr Asn Ile Ile Leu Arg Gly Ile Asp Met Ile 580 585 590	1776
20	GAA TTT CCA AAG AAG ATT GCC AAA AAT GCT GCT AAT TTA ATT AAA AAA Glu Phe Pro Lys Lys Ile Ala Lys Asn Ala Ala Asn Leu Ile Lys Lys 595 600 605	1824
25	CTA TGC AGG GAC AAT CCA TCA GAA AGA TTA GGG AAT TTG AAA AAT GGA Leu Cys Arg Asp Asn Pro Ser Glu Arg Leu Gly Asn Leu Lys Asn Gly 610 615 620	1872
30	GTA AAA GAC ATT CAA AAG CAC AAA TGG TTT GAG GGC TTT AAC TGG GAA Val Lys Asp Ile Gln Lys His Lys Trp Phe Glu Gly Phe Asn Trp Glu 625 630 635 640	1920
35	GGC TTA AGA AAA GGT ACC TTG ACA CCT CCT ATA ATA CCA AGT GTT GCA Gly Leu Arg Lys Gly Thr Leu Thr Pro Pro Ile Ile Pro Ser Val Ala 645 650 655	1968
40	TCA CCC ACA GAC ACA AGT AAT TTT GAC AGT TTC CCT GAG GAC AAC GAT Ser Pro Thr Asp Thr Ser Asn Phe Asp Ser Phe Pro Glu Asp Asn Asp 660 665 670	2016
45	GAA CCA CCA CCT GAT GAC AAC TCA GGA TGG GAT ATA GAC TTC TCG GAT Glu Pro Pro Asp Asp Asn Ser Gly Trp Asp Ile Asp Phe Ser Asp 675 680 685	2064
50	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly 690 695 700	2112
55	GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys 705 710 715 720	2160
55	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu 725 730 735	2208
55	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro 740 745 750	2256

280

	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr 755 760 765	2304
5	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu 770 775 780	2352
10	GCG TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr 785 790 795 800	2400
15	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg 805 810 815	2448
20	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly 820 825 830	2496
	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala 835 840 845	2544
25	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn 850 855 860	2592
30	ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr 865 870 875 880	2640
35	CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser 885 890 895	2688
40	ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met 900 905 910	2736
	GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp 915 920 925	2784
45	GAG CTG TAC AA GTAA Glu Leu Tyr Lys 930	2799
50	(2) INFORMATION FOR SEQ ID NO:137:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 932 amino acids	
55	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	

280

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	Ala	Leu	Gln	Glu	Lys	Ile	Glu
1							5					10			15	
10	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	Asp	Glu	Leu	Glu	Leu	Glu	Leu
							20				25			30		
	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Lys
							35				40			45		
15	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	Gln	Gln	Ala	Gln	Lys	Gln	Ser
							50				55			60		
	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	Thr	Lys	Arg	Gln	Ala	Ile	Ser
							65				70			75		80
	Ala	Glu	Pro	Thr	Ala	Phe	Asp	Ile	Gln	Asp	Leu	Ser	His	Val	Thr	Leu
							85				90			95		
20	Pro	Phe	Tyr	Pro	Lys	Ser	Pro	Gln	Ser	Lys	Asp	Leu	Ile	Lys	Glu	Ala
							100				105			110		
	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn	Leu	Glu	Leu	Ser	Gln	Ile	Gln
							115				120			125		
25	Glu	Ile	Val	Asp	Cys	Met	Tyx	Pro	Val	Glu	Tyr	Gly	Lys	Asp	Ser	Cys
							130				135			140		
	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser	Leu	Val	Tyr	Val	Met	Glu	Asp
							145				150			155		160
	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly	Val	Lys	Leu	Cys	Thr	Met	Gly
							165				170			175		
30	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala	Ile	Leu	Tyr	Asn	Cys	Thr	Arg
							180				185			190		
	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn	Val	Lys	Leu	Trp	Ala	Ile	Asp
							195				200			205		
35	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met	Arg	Thr	Gly	Leu	Ile	Lys	His
							210				215			220		
	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser	Val	Pro	Thr	Phe	Gln	Ser	Leu
							225				230			235		240
	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala	Asp	Val	Leu	Glu	Glu	Thr	His
							245				250			255		
40	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	Gln	Gly	Ala	Arg	Gly	Asp	Thr
							260				265			270		
	Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val	Asn	Val	Thr	Arg	Glu	Asp	Ser
							275				280			285		
45	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg	Thr	Leu	Gly	Lys	Gly	Asp	Trp
							290				295			300		
	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu	Asp	Val	Arg	Thr	Ala	Asn	Val
							305				310			315		320
	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu	Val	Ile	Asp	Arg	Asp	Ser	Phe
							325				330			335		
50	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp	Val	Ser	Asn	Lys	Ala	Tyr	Glu
							340				345			350		
	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu	Ala	Glu	Ala	Ala	Phe	Phe	Ala
							355				360			365		
55	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile	Ile	Asp	Thr	Leu	Gly	Val	Gly
							370				375			380		
	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln	Leu	Lys	Ser	Glu	Glu	Ser	Lys

	385	390	395	400
	Thr Phe Ala Met Lys Ile Leu Lys Lys Arg His Ile Val Asp Thr Arg			
	405	410	415	
5	Gln Gln Glu His Ile Arg Ser Glu Lys Gln Ile Met Gln Gly Ala His			
	420	425	430	
	Ser Asp Phe Ile Val Arg Leu Tyr Arg Thr Phe Lys Asp Ser Lys Tyr			
	435	440	445	
	Leu Tyr Met Leu Met Glu Ala Cys Leu Gly Gly Leu Trp Thr Ile			
	450	455	460	
10	Leu Arg Asp Arg Gly Ser Phe Glu Asp Ser Thr Thr Arg Phe Tyr Thr			
	465	470	475	480
	Ala Cys Val Val Glu Ala Phe Ala Tyr Leu His Ser Lys Gly Ile Ile			
	485	490	495	
	Tyr Arg Asp Leu Lys Pro Glu Asn Leu Ile Leu Asp His Arg Gly Tyr			
15	500	505	510	
	Ala Lys Leu Val Asp Phe Gly Phe Ala Lys Lys Ile Gly Phe Gly Lys			
	515	520	525	
	Lys Thr Trp Thr Phe Cys Gly Thr Pro Glu Tyr Val Ala Pro Glu Ile			
	530	535	540	
20	Ile Leu Asn Lys Gly His Asp Ile Ser Ala Asp Tyr Trp Ser Leu Gly			
	545	550	555	560
	Ile Leu Met Tyr Glu Leu Leu Thr Gly Ser Pro Pro Phe Ser Gly Pro			
	565	570	575	
	Asp Pro Met Lys Thr Tyr Asn Ile Ile Leu Arg Gly Ile Asp Met Ile			
25	580	585	590	
	Glu Phe Pro Lys Lys Ile Ala Lys Asn Ala Ala Asn Leu Ile Lys Lys			
	595	600	605	
	Leu Cys Arg Asp Asn Pro Ser Glu Arg Leu Gly Asn Leu Lys Asn Gly			
	610	615	620	
30	Val Lys Asp Ile Gln Lys His Lys Trp Phe Glu Gly Phe Asn Trp Glu			
	625	630	635	640
	Gly Leu Arg Lys Gly Thr Leu Thr Pro Pro Ile Ile Pro Ser Val Ala			
	645	650	655	
	Ser Pro Thr Asp Thr Ser Asn Phe Asp Ser Phe Pro Glu Asp Asn Asp			
35	660	665	670	
	Glu Pro Pro Pro Asp Asp Asn Ser Gly Trp Asp Ile Asp Phe Ser Asp			
	675	680	685	
	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly			
	690	695	700	
40	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys			
	705	710	715	720
	Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu			
	725	730	735	
	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro			
45	740	745	750	
	Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr			
	755	760	765	
	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu			
	770	775	780	
50	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr			
	785	790	795	800
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg			
	805	810	815	
	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly			
55	820	825	830	
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala			

283

	835	840	845
	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn		
	850	855	860
	Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr		
5	865	870	875
	Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser		880
	885	890	895
	Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met		
	900	905	910
10	val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp		
	915	920	925
	Glu Leu Tyr Lys		
	930		

15 (2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2184 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 25
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2181
 - (D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
35			
GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96		
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
40			
GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144		
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
45			
TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192		
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
50			
CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240		
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80
55			
CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288		
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
55			
CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336		

283

284

	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100	105	110
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC		384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
	115	120	125
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC		432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
	130	135	140
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC		480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
	145	150	155
	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC		528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
	165	170	175
20	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC		576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
	180	185	190
25	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG		624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
	195	200	205
30	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC		672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
	210	215	220
35	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC		720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
	225	230	235
40	GGA CTC AGA TCT CGA GGC ACC ATG AGC GAC GTG GCT ATT GTG AAG GAG		768
	Gly Leu Arg Ser Arg Gly Thr Met Ser Asp Val Ala Ile Val Lys Glu		
	245	250	255
45	GGT TGG CTG CAC AAA CGA GGG GAG TAC ATC AAG ACC TGG CGG CCA CGC		816
	Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro Arg		
	260	265	270
50	TAC TTC CTC CTC AAG AAT GAT GGC ACC TTC ATT GGC TAC AAG GAG CGG		864
	Tyr Phe Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg		
	275	280	285
55	CCG CAG GAT GTG GAC CAA CGT GAG GCT CCC CTC AAC AAC TTC TCT GTG		912
	Pro Gln Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn Phe Ser Val		
	290	295	300
	GC G CAG TGC CAG CTG ATG AAG ACG GAG CGG CCC CGG CCC AAC ACC TTC		960
	Ala Gln Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe		
	305	310	315
	ATC ATC CGC TGC CTG CAG TGG ACC ACT GTC ATC GAA CGC ACC TTC CAT		1008

284

285

	Ile Ile Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His		
	325	330	335
5	GTG GAG ACT CCT GAG GAG CGG GAG GAG TGG ACA ACC GCC ATC CAG ACT Val Glu Thr Pro Glu Glu Arg Glu Trp Thr Thr Ala Ile Gln Thr		1056
	340	345	350
10	GTG GCT GAC GGC CTC AAG AAG CAG GAG GAG GAG ATG GAC TTC CGG Val Ala Asp Gly Leu Lys Lys Gln Glu Glu Glu Met Asp Phe Arg		1104
	355	360	365
15	TCG GGC TCA CCC AGT GAC AAC TCA GGG GCT GAA GAG ATG GAG GTG TCC Ser Gly Ser Pro Ser Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser		1152
	370	375	380
20	CTG GCC AAG CCC AAG CAC CGC GTG ACC ATG AAC GAG TTT GAG TAC CTG Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu		1200
	385	390	395
	400		
25	AAG CTG CTG GGC AAG GGC ACT TTC GGC AAG GTG ATC CTG GTG AAG GAG Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu		1248
	405	410	415
30	AAG GCC ACA GGC CGC TAC TAC GCC ATG AAG ATC CTC AAG AAG GAA GTC Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val		1296
	420	425	430
35	ATC GTG GCC AAG GAC GAG GTG GCC CAC ACA CTC ACC GAG AAC CGC GTC Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val		1344
	435	440	445
40	CTG CAG AAC TCC AGG CAC CCC TTC CTC ACA GCC CTG AAG TAC TCT TTC Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe		1392
	450	455	460
45	CAG ACC CAC GAC CGC CTC TGC TTT GTC ATG GAG TAC GCC AAC GGG GGC Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly		1440
	465	470	475
	480		
50	GAG CTG TTC TTC CAC CTG TCC CGG GAA CGT GTG TTC TCC GAG GAC CGG Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg		1488
	485	490	495
55	GCC CGC TTC TAT GGC GCT GAG ATT GTG TCA GCC CTG GAC TAC CTG CAC Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His		1536
	500	505	510
60	TCG GAG AAG AAC GTG GTG TAC CGG GAC CTC AAG CTG GAG AAC CTC ATG Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met		1584
	515	520	525
65	CTG GAC AAG GAC GGG CAC ATT AAG ATC ACA GAC TTC GGG CTG TGC AAG Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys		1632
	530	535	540
70	GAG GGG ATC AAG GAC GGT GCC ACC ATG AAG ACC TTT TGC GGC ACA CCT		1680

286

	Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro			
545	550	555	560	
	GAG TAC CTG GCC CCC GAG GTG CTG GAG GAC AAT GAC TAC GGC CGT GCA		1728	
5	Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala			
	565	570	575	
	GTG GAC TGG TGG GGG CTG GGC GTG GTC ATG TAC GAG ATG ATG TGC GGT		1776	
10	Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly			
	580	585	590	
	CGC CTG CCC TTC TAC AAC CAG GAC CAT GAG AAG CTT TTT GAG CTC ATC		1824	
	Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile			
	595	600	605	
15	CTC ATG GAG GAG ATC CGC TTC CCG CGC ACG CTT GGT CCC GAG GCC AAG		1872	
	Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys			
	610	615	620	
20	TCC TTG CTT TCA GGG CTG CTC AAG AAG GAC CCC AAG CAG AGG CTT GGC		1920	
	Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly			
	625	630	635	640
25	GGG GGC TCC GAG GAC GCC AAG GAG ATC ATG CAG CAT CGC TTC TTT GCC		1968	
	Gly Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala			
	645	650	655	
30	GGT ATC GTG TGG CAG CAC GTG TAC GAG AAG AAG CTC AGC CCA CCC TTC		2016	
	Gly Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe			
	660	665	670	
	AAG CCC CAG GTC ACG TCG GAG ACT GAC ACC AGG TAT TTT GAT GAG GAG		2064	
	Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu			
	675	680	685	
35	TTC ACG GCC CAG ATG ATC ACC ATC ACA CCA CCT GAC CAA GAT GAC AGC		2112	
	Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser			
	690	695	700	
40	ATG GAG TGT GTG GAC AGC GAG CGC AGG CCC CAC TTC CCC CAG TTC TCC		2160	
	Met Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser			
	705	710	715	720
45	TAC TCG GCC AGC AGC ACG GCC TGA		2184	
	Tyr Ser Ala Ser Ser Thr Ala			
	725			

(2) INFORMATION FOR SEQ ID NO:139:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 727 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
	20	25	30	
10	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	35	40	45	
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
	50	55	60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
15	65	70	75	80
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
	85	90	95	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
	100	105	110	
20	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
	115	120	125	
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
	130	135	140	
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
25	145	150	155	160
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
	165	170	175	
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
	180	185	190	
30	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
	195	200	205	
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
	210	215	220	
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
35	225	230	235	240
	Gly Leu Arg Ser Arg Gly Thr Met Ser Asp Val Ala Ile Val Lys Glu			
	245	250	255	
	Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro Arg			
	260	265	270	
40	Tyr Phe Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg			
	275	280	285	
	Pro Gln Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn Phe Ser Val			
	290	295	300	
	Ala Gln Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe			
45	305	310	315	320
	Ile Ile Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His			
	325	330	335	
	Val Glu Thr Pro Glu Glu Arg Glu Glu Trp Thr Thr Ala Ile Gln Thr			
	340	345	350	
50	Val Ala Asp Gly Leu Lys Lys Gln Glu Glu Glu Glu Met Asp Phe Arg			
	355	360	365	
	Ser Gly Ser Pro Ser Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser			
	370	375	380	
	Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu			
55	385	390	395	400
	Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu			

288

	405	410	415
	Lys Ala Thr Gly Arg Tyr Tyr Ala Met	Lys Ile Leu Lys Lys Glu Val	
	420	425	430
5	Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val		
	435	440	445
	Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe		
	450	455	460
10	Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly		
	465	470	475
	Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg		
	485	490	495
	Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His		
	500	505	510
15	Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met		
	515	520	525
	Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys		
	530	535	540
20	Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro		
	545	550	555
	Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala		
	565	570	575
	Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly		
	580	585	590
25	Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile		
	595	600	605
	Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys		
	610	615	620
30	Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly		
	625	630	635
	Gly Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala		
	645	650	655
	Gly Ile Val Trp Gln His Val Tyr Glu Lys Leu Ser Pro Pro Phe		
	660	665	670
35	Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu		
	675	680	685
	Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser		
	690	695	700
	Met Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser		
	705	710	715
40	Tyr Ser Ala Ser Ser Thr Ala		
	725		

(2) INFORMATION FOR SEQ ID NO:140:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA
- 55 (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2391
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

	ATG GAC GAA CTG TTC CCC CTC ATC TTC CCG GCA GAG CCA GCC CAG GCC	48
5	Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala	
	1 5 10 15	
	TCT GGC CCC TAT GTG GAG ATC ATT GAG CAG CCC AAG CAG CGG GGC ATG	96
10	Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met	
	20 25 30	
	CGC TTC CGC TAC AAG TGC GAG GGG CGC TCC GCG GGC AGC ATC CCA GGC	144
	Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly	
	35 40 45	
15	GAG AGG AGC ACA GAT ACC ACC AAG ACC CAC CCC ACC ATC AAG ATC AAT	192
	Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn	
	50 55 60	
20	GGC TAC ACA GGA CCA GGG ACA GTG CGC ATC TCC CTG GTC ACC AAG GAC	240
	Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp	
	65 70 75 80	
25	CCT CCT CAC CGG CCT CAC CCC CAC GAG CTT GTA GGA AAG GAC TGC CGG	288
	Pro Pro His Arg Pro His Pro Glu Leu Val Gly Lys Asp Cys Arg	
	85 90 95	
30	GAT GGC TTC TAT GAG GCT GTC CTC TGC CCG GAC CGC TGC ATC CAC AGT	336
	Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser	
	100 105 110	
35	TTC CAG AAC CTG GGA ATC CAG TGT GTG AAG AAG CGG GAC CTG GAG CAG	384
	Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln	
	115 120 125	
	GCT ATC AGT CAG CGC ATC CAG ACC AAC AAC AAC CCC TTC CAA GTT CCT	432
	Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro	
	130 135 140	
40	ATA GAA GAG CAG CGT GGG GAC TAC GAC CTG AAT GCT GTG CGG CTC TGC	480
	Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys	
	145 150 155 160	
45	TTC CAG GTG ACA GTG CGG GAC CCA TCA GGC AGG CCC CTC CGC CTG CCG	528
	Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro	
	165 170 175	
	CCT GTC CTT CCT CAT CCC ATC TTT GAC AAT CGT GCC CCC AAC ACT GCC	576
	Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala	
50	180 185 190	
	GAG CTC AAG ATC TGC CGA GTG AAC CGA AAC TCT GGC AGC TGC CTC GGT	624
	Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly	
	195 200 205	
55	GGG GAT GAG ATC TTC CTA CTG TGT GAC AAG GTG CAG AAA GAG GAC ATT	672

290

	Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile		
210	215	220	
5	GAG GTG TAT TTC ACG GGA CCA GGC TGG GAG GCC CGA GGC TCC TTT TCG Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser		720
225	230	235	240
10	CAA GCT GAT GTG CAC CGA CAA GTG GCC ATT GTG TTC CGG ACC CCT CCC Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro		768
245	250	255	
15	TAC GCA GAC CCC AGC CTG CAG GCT CCT GTG CGT GTC TCC ATG CAG CTG Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu		816
260	265	270	
20	275	280	285
25	CGG CGG CCT TCC GAC CGG GAG CTC AGT GAG CCC ATG GAA TTC CAG TAC Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr		864
290	295	300	
30	325	330	335
35	ACA TAT GAG ACC TTC AAG AGC ATC ATG AAG AAG AGT CCT TTC AGC GGA Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly		960
305	310	315	320
40	340	345	350
45	CCC ACC GAC CCC CGG CCT CCA CCT CGA CGC ATT GCT GTG CCT TCC CGC Pro Thr Asp Pro Arg Pro Pro Arg Arg Ile Ala Val Pro Ser Arg		1008
325	330	335	
50	340	345	350
55	TCA TCC CTG AGC ACC ATC AAC TAT GAT GAG TTT CCC ACC ATG GTG TTT Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe		1056
355	360	365	
60	370	375	380
65	385	390	395
70	405	410	415
75	420	425	430
80	440	445	450
85	460	465	470
90	480	485	490
95	500	505	510
100	520	525	530
105	540	545	550
110	560	565	570
115	580	585	590
120	600	605	610
125	620	625	630
130	640	645	650
135	660	665	670
140	680	685	690
145	700	705	710
150	720	725	730
155	740	745	750
160	760	765	770
165	780	785	790
170	800	805	810
175	820	825	830
180	840	845	850
185	860	865	870
190	880	885	890
195	900	905	910
200	920	925	930
205	940	945	950
210	960	965	970
215	980	985	990
220	1000	1005	1010
225	1020	1025	1030
230	1040	1045	1050
235	1060	1065	1070
240	1080	1085	1090
245	1100	1105	1110
250	1120	1125	1130
255	1140	1145	1150
260	1160	1165	1170
265	1180	1185	1190
270	1200	1205	1210
275	1220	1225	1230
280	1240	1245	1250
285	1260	1265	1270
290	1280	1285	1290
295	1300	1305	1310
300	1320	1325	1330
305	1340	1345	1350
310	1360	1365	1370
315	1380	1385	1390
320	1400	1405	1410
325	1420	1425	1430
330	1440	1445	1450
335	1460	1465	1470
340	1480	1485	1490
345	1500	1505	1510
350	1520	1525	1530
355	1540	1545	1550
360	1560	1565	1570
365	1580	1585	1590
370	1600	1605	1610
375	1620	1625	1630
380	1640	1645	1650
385	1660	1665	1670
390	1680	1685	1690
395	1700	1705	1710
400	1720	1725	1730
405	1740	1745	1750
410	1760	1765	1770
415	1780	1785	1790
420	1800	1805	1810
425	1820	1825	1830
430	1840	1845	1850
435	1860	1865	1870
440	1880	1885	1890
445	1900	1905	1910
450	1920	1925	1930
455	1940	1945	1950
460	1960	1965	1970
465	1980	1985	1990
470	2000	2005	2010
475	2020	2025	2030
480	2040	2045	2050
485	2060	2065	2070
490	2080	2085	2090
495	2100	2105	2110
500	2120	2125	2130
505	2140	2145	2150
510	2160	2165	2170
515	2180	2185	2190
520	2200	2205	2210
525	2220	2225	2230
530	2240	2245	2250
535	2260	2265	2270
540	2280	2285	2290
545	2300	2305	2310
550	2320	2325	2330
555	2340	2345	2350
560	2360	2365	2370
565	2380	2385	2390
570	2400	2405	2410
575	2420	2425	2430
580	2440	2445	2450
585	2460	2465	2470
590	2480	2485	2490
595	2500	2505	2510
600	2520	2525	2530
605	2540	2545	2550
610	2560	2565	2570
615	2580	2585	2590
620	2600	2605	2610
625	2620	2625	2630
630	2640	2645	2650
635	2660	2665	2670
640	2680	2685	2690
645	2700	2705	2710
650	2720	2725	2730
655	2740	2745	2750
660	2760	2765	2770
665	2780	2785	2790
670	2800	2805	2810
675	2820	2825	2830
680	2840	2845	2850
685	2860	2865	2870
690	2880	2885	2890
695	2900	2905	2910
700	2920	2925	2930
705	2940	2945	2950
710	2960	2965	2970
715	2980	2985	2990
720	3000	3005	3010
725	3020	3025	3030
730	3040	3045	3050
735	3060	3065	3070
740	3080	3085	3090
745	3100	3105	3110
750	3120	3125	3130
755	3140	3145	3150
760	3160	3165	3170
765	3180	3185	3190
770	3200	3205	3210
775	3220	3225	3230
780	3240	3245	3250
785	3260	3265	3270
790	3280	3285	3290
795	3300	3305	3310
800	3320	3325	3330
805	3340	3345	3350
810	3360	3365	3370
815	3380	3385	3390
820	3400	3405	3410
825	3420	3425	3430
830	3440	3445	3450
835	3460	3465	3470
840	3480	3485	3490
845	3500	3505	3510
850	3520	3525	3530
855	3540	3545	3550
860	3560	3565	3570
865	3580	3585	3590
870	3600	3605	3610
875	3620	3625	3630
880	3640	3645	3650
885	3660	3665	3670
890	3680	3685	3690
895	3700	3705	3710
900	3720	3725	3730
905	3740	3745	3750
910	3760	3765	3770
915	3780	3785	3790
920	3800	3805	3810
925	3820	3825	3830
930	3840	3845	3850
935	3860	3865	3870
940	3880	3885	3890
945	3900	3905	3910
950	3920	3925	3930
955	3940	3945	3950
960	3960	3965	3970
965	3980	3985	3990
970	4000	4005	4010
975	4020	4025	4030
980	4040	4045	4050
985	4060	4065	4070
990	4080	4085	4090
995	4100	4105	4110
1000	4120	4125	4130
1005	4140	4145	4150
1010	4160	4165	4170
1015	4180	4185	4190
1020	4200	4205	4210
1025	4220	4225	4230
1030	4240	4245	4250
1035	4260	4265	4270
1040	4280	4285	4290
1045	4300	4305	4310
1050	4320	4325	4330
1055	4340	4345	4350
1060	4360	4365	4370
1065	4380	4385	4390
1070	4400	4405	4410
1075	4420	4425	4430
1080	4440	4445	4450
1085	4460	4465	4470
1090	4480	4485	4490
1095	4500	4505	4510
1100	4520	4525	4530
1105	4540	4545	4550
1110	4560	4565	4570
1115	4580	4585	4590
1120	4600	4605	4610
1125	4620	4625	4630
1130	4640	4645	4650
1135	4660	4665	4670
1140	4680	4685	4690
1145	4700	4705	4710
1150	4720	4725	4730
1155	4740	4745	4750
1160	4760	4765	4770
1165	4780	4785	4790
1170	4800	4805	4810
1175	4820	4825	4830
1180	4840	4845	4850
1185	4860	4865	4870
1190	4880	4885	4890
1195	4900	4905	4910
1200	4920	4925	4930
1205	4940	4945	4950
1210	4960	4965	4970
1215	4980	4985	4990
1220	5000	5005	5010
1225	5020	5025	5030
1230	5040	5045	5050
1235	5060	5065	5070
1240	5080	5085	5090
1245	5100	5105	5110
1250	5120	5125	5130
1255	5140	5145	5150
1260	5160	5165	5170
1265	5180	5185	5190
1270	5200	5205	5210
1275	5220	5225	5230
1280	5240	5245	5250
1285	5260	5265	5270
1290	5280	5285	5290
1295	5300	5305	5310
1300	5320	5325	5330
1305	5340	5345	5350
1310	5360	5365	5370
1315	5380	5385	5390
1320	5400	5405	5410
1325	5420	5425	5430
1330	5440	5445	5450
1335	5460	5465	5470
1340	5480	5485	5490
1345	5500</td		

291

	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	Leu	Gln	Phe	Asp	Asp	Glu	
	435						440						445				
5	GAC	CTG	GGG	GCC	TTG	CTT	GGC	AAC	AGC	ACA	GAC	CCA	GCT	GTG	TTC	ACA	1392
	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr	Asp	Pro	Ala	Val	Phe	Thr	
	450						455					460					
10	GAC	CTG	GCA	TCC	GTC	GAC	AAC	TCC	GAG	TTT	CAG	CAG	CTG	CTG	AAC	CAG	1440
	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	Gln	Gln	Leu	Leu	Asn	Gln	
	465						470				475		480				
15	GGC	ATA	CCT	GTG	GCC	CCC	CAC	ACA	ACT	GAG	CCC	ATG	CTG	ATG	GAG	TAC	1488
	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	Pro	Met	Leu	Met	Glu	Tyr	
	485						490					495					
20	CCT	GAG	GCT	ATA	ACT	CGC	CTA	GTG	ACA	GGG	GCC	CAG	AGG	CCC	CCC	GAC	1536
	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	Ala	Gln	Arg	Pro	Pro	Asp	
	500						505					510					
25	CCA	GCT	CCT	GCT	CCA	CTG	GGG	GCC	CCG	GGG	CTC	CCC	AAT	GGC	CTC	CTT	1584
	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly	Leu	Pro	Asn	Gly	Leu	Leu	
	515						520					525					
30	TCA	GGA	GAT	GAA	GAC	TTC	TCC	ATT	GCG	GAC	ATG	GAC	TTC	TCA	GCC		1632
	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala	Asp	Met	Asp	Phe	Ser	Ala	
	530						535					540					
35	CTG	CTG	AGT	CAG	ATC	AGC	TCC	TTG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	1680
	Leu	Leu	Ser	Gln	Ile	Ser	Ser	Leu	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	
	545						550					555				560	
40	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	1728
	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
	565						570					575					
45	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	1776
	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
	580						585					590					
50	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	1824
	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	
	595						600					605					
55	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	1872
	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	
	610						615					620					
60	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	1920
	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	
	625						630					635				640	
65	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	1968
	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	
	645						650					655					
70	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	2016

292

	Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			
	660	665	670	
5	TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC		2064	
	Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
	675	680	685	
10	TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC		2112	
	Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr			
	690	695	700	
15	AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAC GGC ATC		2160	
	Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile			
	705	710	715	720
20	AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG		2208	
	Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln			
	725	730	735	
25	CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG		2256	
	Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
	740	745	750	
30	CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA		2304	
	Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
	755	760	765	
35	GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC		2352	
	Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr			
	770	775	780	
40	GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA		2394	
	Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
	785	790	795	

(2) INFORMATION FOR SEQ ID NO:141:

	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 797 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: protein	
	(v) FRAGMENT TYPE: internal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:	
50	Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala	
	1 5 10 15	
	Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met	
	20 25 30	
55	Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly	
	35 40 45	
	Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn	

292

	50	55	60													
	Gly	Tyr	Thr	Gly	Pro	Gly	Thr	Val	Arg	Ile	Ser	Leu	Val	Thr	Lys	Asp
	65			70			75			80						
5	Pro	Pro	His	Arg	Pro	His	Pro	His	Glu	Leu	Val	Gly	Lys	Asp	Cys	Arg
	85				90				95							
	Asp	Gly	Phe	Tyr	Glu	Ala	Glu	Leu	Cys	Pro	Asp	Arg	Cys	Ile	His	Ser
	100				105				110							
10	Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Arg	Asp	Leu	Glu	Gln
	115			120				125								
15	Ala	Ile	Ser	Gln	Arg	Ile	Gln	Thr	Asn	Asn	Asn	Pro	Phe	Gln	Val	Pro
	130			135			140									
	Ile	Glu	Glu	Gln	Arg	Gly	Asp	Tyr	Asp	Leu	Asn	Ala	Val	Arg	Leu	Cys
	145			150			155			160						
20	Phe	Gln	Val	Thr	Val	Arg	Asp	Pro	Ser	Gly	Arg	Pro	Leu	Arg	Leu	Pro
	165			170			175									
	Pro	Val	Leu	Pro	His	Ile	Phe	Asp	Asn	Arg	Ala	Pro	Asn	Thr	Ala	
	180			185			190									
	Glu	Leu	Lys	Ile	Cys	Arg	Val	Asn	Arg	Asn	Ser	Gly	Ser	Cys	Leu	Gly
	195			200			205									
25	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Glu	Asp	Ile
	210			215			220									
	Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	Ala	Arg	Gly	Ser	Phe	Ser
	225			230			235			240						
30	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro
	245			250			255									
	Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val	Arg	Val	Ser	Met	Gln	Leu
	260			265			270									
	Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu	Pro	Met	Glu	Phe	Gln	Tyr
	275			280			285									
35	Leu	Pro	Asp	Thr	Asp	Asp	Arg	His	Arg	Ile	Glu	Glu	Lys	Arg	Lys	Arg
	290			295			300									
	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	Lys	Ser	Pro	Phe	Ser	Gly
	305			310			315			320						
40	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Arg	Arg	Ile	Ala	Val	Pro	Ser	Arg	
	325			330			335									
	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	Gln	Pro	Tyr	Pro	Phe	Thr
	340			345			350									
	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	Phe	Pro	Thr	Met	Val	Phe
	355			360			365									
45	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	Leu	Ala	Pro	Ala	Pro	Pro
	370			375			380									
	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Met	Val
	385			390			395			400						
	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	Pro	Val	Leu	Ala	Pro	Gly
	405			410			415									
	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	Lys	Pro	Thr	Gln	Ala	Gly
	420			425			430									
	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	Leu	Gln	Phe	Asp	Asp	Glu
	435			440			445									
50	Asp	Leu	Gly	Ala	Leu	Gly	Asn	Ser	Thr	Asp	Pro	Ala	Val	Phe	Thr	
	450			455			460									
	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	Gln	Gln	Leu	Leu	Asn	Gln
	465			470			475			480						
55	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	Pro	Met	Leu	Met	Glu	Tyr
	485			490			495									
	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	Ala	Gln	Arg	Pro	Pro	Asp

294

	500	505	510
	Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu		
	515	520	525
5	Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala		
	530	535	540
	Leu Leu Ser Gln Ile Ser Ser Leu Asp Pro Pro Val Ala Thr Met Val		
	545	550	555
	Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu		
	565	570	575
10	Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly		
	580	585	590
	Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr		
	595	600	605
15	Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr		
	610	615	620
	Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His		
	625	630	635
	Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr		
	645	650	655
20	Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys		
	660	665	670
	Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp		
	675	680	685
	Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr		
25	690	695	700
	Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile		
	705	710	715
	Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln		
	725	730	735
30	Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val		
	740	745	750
	Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys		
	755	760	765
35	Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr		
	770	775	780
	Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	785	790	795

(2) INFORMATION FOR SEQ ID NO:142:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

50

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2391

(D) OTHER INFORMATION:

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG

48

294

295

	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10	15
5	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		96
	20	25	30
10	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		144
	35	40	45
15	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		192
	50	55	60
20	55	60	
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		240
	65	70	75
30	75	80	
35	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		288
	85	90	95
40			
45	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		336
	100	105	110
50			
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		384
	115	120	125
60			
65	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		432
	130	135	140
70			
75	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		480
	145	150	155
80	155	160	
85			
90	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		528
	165	170	175
95			
100	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		576
	180	185	190
105			
110	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		624
	195	200	205
115			
120	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		672
	210	215	220
125			
130	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC		720
			295

296

	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
225	230	235	240
5	GGA CTC AGA TCT CGA GCC ATG GAC GAA CTG TTC CCC CTC ATC TTC CCG Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro		768
	245	250	255
10	GCA GAG CCA GCC CAG GCC TCT GGC CCC TAT GTG GAG ATC ATT GAG CAG Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln		816
	260	265	270
15	CCC AAG CAG CGG GGC ATG CGC TTC CGC TAC AAG TGC GAG GGG CGC TCC Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser		864
	275	280	285
20	GCG GGC AGC ATC CCA GGC GAG AGG AGC ACA GAT ACC ACC AAG ACC CAC Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His		912
	290	295	300
25	CCC ACC ATC AAG ATC AAT GGC TAC ACA GGA CCA GGG ACA GTG CGC ATC Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile		960
	305	310	315
	320		
30	TCC CTG GTC ACC AAG GAC CCT CCT CAC CGG CCT CAC CCC CAC GAG CTT Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu		1008
	325	330	335
35	GTA GGA AAG GAC TGC CGG GAT GGC TTC TAT GAG GCT GAG CTC TGC CCG Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro		1056
	340	345	350
40	GAC CGC TGC ATC CAC AGT TTC CAG AAC CTG GGA ATC CAG TGT GTG AAG Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys		1104
	355	360	365
45	AAG CGG GAC CTG GAG CAG GCT ATC AGT CAG CGC ATC CAG ACC AAC AAC Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn		1152
	370	375	380
50	AAC CCC TTC CAA GTT CCT ATA GAA GAG CAG CGT GGG GAC TAC GAC CTG Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu		1200
	385	390	395
	400		
55	AAT GCT GTG CGG CTC TGC TTC CAG GTG ACA GTG CGG GAC CCA TCA GGC Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly		1248
	405	410	415
60	AGG CCC CTC CGC CTG CCG CCT GTC CTT CCT CAT CCC ATC TTT GAC AAT Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn		1296
	420	425	430
65	CGT GCC CCC AAC ACT GCC GAG CTC AAG ATC TGC CGA GTG AAC CGA AAC Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn		1344
	435	440	445
70	TCT GGC AGC TGC CTC GGT GGG GAT GAG ATC TTC CTA CTG TGT GAC AAG		1392

297

	Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys		
	450	455	460
5	GTG CAG AAA GAG GAC ATT GAG GTG TAT TTC ACG GGA CCA GGC TGG GAG Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu		1440
	465	470	475
10	GCC CGA GGC TCC TTT TCG CAA GCT GAT GTG CAC CGA CAA GTG GCC ATT Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile		1488
	485	490	495
15	GTG TTC CGG ACC CCT CCC TAC GCA GAC CCC AGC CTG CAG GCT CCT GTG Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val		1536
	500	505	510
20	CGT GTC TCC ATG CAG CTG CGG CGG CCT TCC GAC CGG GAG CTC AGT GAG Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu		1584
	515	520	525
25	CCC ATG GAA TTC CAG TAC CTG CCA GAT ACA GAC GAT CGT CAC CGG ATT Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile		1632
	530	535	540
30	GAG GAG AAA CGT AAA AGG ACA TAT GAG ACC TTC AAG AGC ATC ATG AAG Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys		1680
	545	550	555
35	AAG AGT CCT TTC AGC GGA CCC ACC GAC CCC CGG CCT CCA CCT CGA CGC Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg		1728
	565	570	575
40	ATT GCT GTG CCT TCC CGC AGC TCA GCT TCT GTC CCC AAG CCA GCA CCC Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro		1776
	580	585	590
45	CAG CCC TAT CCC TTT ACG TCA TCC CTG AGC ACC ATC AAC TAT GAT GAG Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu		1824
	595	600	605
50	TTT CCC ACC ATG GTG TTT CCT TCT GGG CAG ATC AGC CAG GCC TCG GCC Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala		1872
	610	615	620
55	TTG GCC CCG GCC CCT CCC CAA GTC CTG CCC CAG GCT CCA GCC CCT GCC Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala		1920
	625	630	635
60	CCT GCT CCA GCC ATG GTA TCA GCT CTG GCC CAG GCC CCA GCC CCT GTC Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val		1968
	645	650	655
65	CCA GTC CTA GCC CCA GGC CCT CCT CAG GCT GTG GCC CCA CCT GCC CCC Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro		2016
	660	665	670
70	AAG CCC ACC CAG GCT GGG GAA GGA ACG CTG TCA GAG GCC CTG CTG CAG		2064

298

	Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln		
	675	680	685
5	CTG CAG TTT GAT GAT GAA GAC CTG GGG GCC TTG CTT GGC AAC AGC ACA		2112
	Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr		
	690	695	700
10	GAC CCA GCT GTG TTC ACA GAC CTG GCA TCC GTC GAC AAC TCC GAG TTT		2160
	Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe		
	705	710	715
	CAG CAG CTG CTG AAC CAG GGC ATA CCT GTG GCC CCC CAC ACA ACT GAG		2208
	Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu		
	725	730	735
15	CCC ATG CTG ATG GAG TAC CCT GAG GCT ATA ACT CGC CTA GTG ACA GGG		2256
	Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly		
	740	745	750
20	GCC CAG AGG CCC CCC GAC CCA GCT CCT GCT CCA CTG GGG GCC CCG GGG		2304
	Ala Gln Arg Pro Pro Asp Pro Ala Pro Leu Gly Ala Pro Gly		
	755	760	765
25	CTC CCC AAT GGC CTC CTT TCA GGA GAT GAA GAC TTC TCC TCC ATT GCG		2352
	Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala		
	770	775	780
30	GAC ATG GAC TTC TCA GCC CTG CTG AGT CAG ATC AGC TCC TAA		2394
	Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser		
	785	790	795

(2) INFORMATION FOR SEQ ID NO:143:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 797 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
40	(ii) MOLECULE TYPE: protein
	(v) FRAGMENT TYPE: internal
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
	1 5 10 15
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
	20 25 30
50	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
	35 40 45
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
	50 55 60
55	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
	65 70 75 80
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

298

299

	85	90	95
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100	105	110
5	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
	115	120	125
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
	130	135	140
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
	145	150	155
10	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		160
	165	170	175
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
	180	185	190
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
15	195	200	205
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
	210	215	220
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
	225	230	235
20	Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro		240
	245	250	255
	Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln		
	260	265	270
25	Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser		
	275	280	285
	Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His		
	290	295	300
	Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile		
	305	310	315
30	Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu		320
	325	330	335
	Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro		
	340	345	350
35	Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys		
	355	360	365
	Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn		
	370	375	380
	Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu		
	385	390	395
40	Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly		400
	405	410	415
	Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn		
	420	425	430
45	Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn		
	435	440	445
	Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys		
	450	455	460
	Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu		
	465	470	475
50	Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile		480
	485	490	495
	Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val		
	500	505	510
55	Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu		
	515	520	525
	Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile		

300

	530	535	540
	Glu Glu Lys Arg Lys Arg	Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys	
5	545	550	555
	Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Arg Arg		560
	565	570	575
	Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro		
	580	585	590
	Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu		
	595	600	605
10	Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala		
	610	615	620
	Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala		
	625	630	635
	Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val		640
15	645	650	655
	Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro		
	660	665	670
	Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln		
	675	680	685
20	Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr		
	690	695	700
	Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe		
	705	710	715
	Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu		720
25	725	730	735
	Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly		
	740	745	750
	Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly		
	755	760	765
30	Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala		
	770	775	780
	Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser		
	785	790	795

CLAIMS

1. A method for extracting quantitative information relating to an influence on a cellular response, the method comprising recording variation, caused by the influence on a mechanically intact living cell or mechanically intact living cells, in spatially distributed light emitted from a luminophore, the luminophore being present in the cell or cells and being capable of being redistributed in a manner which is related with the degree of the influence, and/or of being modulated by a component which is capable of being redistributed in a manner which is related to the degree of the influence, the association resulting in a modulation of the luminescence characteristics of the luminophore, and processing the recorded variation in the spatially distributed light to provide quantitative information correlating the spatial distribution to the degree of the influence on the cellular response.
5
10
2. A method according to claim 1, as used for extracting quantitative information relating to an influence on an intracellular pathway involving redistribution of at least one component associated with the pathway, or part thereof, the method comprising recording the result of the influence on mechanically intact living cell or cells, as manifested in spatially distributed light emitted from a luminophore which is present in the cell or cells and which is capable of being redistributed, by modulation of the pathway, in a manner which is related to the redistribution of the at least one component of the intracellular pathway, processing the recorded result to provide quantitative information about the spatially distributed light and correlating the quantitative information to the degree of the influence on the intracellular pathway.
15
20
3. A method according to claim 1 or 2, wherein the quantitative information which is indicative of the degree of the cellular response to the influence or the result of the influence on the intracellular pathway is extracted from the recording or recordings according to a predetermined calibration based on responses or results, recorded in the same manner, to known degrees of a relevant specific influence.
25
4. A method according to any of the preceding claims, wherein the influence is contact between the mechanically intact living cell or the group of mechanically intact living cells with a
30

302

chemical substance and/or incubation of the mechanically intact living cell or the group of mechanically intact living cells with a chemical substance.

5. A method according to claim 4 wherein the substance is a substance whose effect on an intracellular pathway is to be determined.
6. A method according to any of the preceding claims, wherein the recording is made at a single point in time after the application of the influence.
- 10 7. A method according to any of claims 1-5, wherein the recording is made at two points in time, one point being before, and the other point being after the application of the influence.
- 15 8. A method according to any of claims 1-5, wherein the recording is performed at a series of points in time, in which the application of the influence occurs at some time after the first time point in the series of recordings, the recording being performed, e.g., with a predetermined time spacing of from 0.1 seconds to 1 hour, preferably from 1 to 60 seconds, more preferably from 1 to 30 seconds, in particular from 1 to 10 seconds, over a time span of from 1 second to 12 hours, such as from 10 seconds to 12 hours, e.g., from 10 seconds to one hour, such as from 60 seconds to 30 minutes or 20 minutes.
- 20 9. A method according to any of claims 1-7, wherein the cell or cells is/are fixed at a point in time after the application of the influence at which the response has been predetermined to be significant, and the recording is made at an arbitrary later time.
- 25 10. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of being redistributed in a manner which is physiologically relevant to the degree of the influence.

11. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of associating with a component which is capable of being redistributed in manner which is physiologically relevant to the degree of the influence.
- 5 12. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of being redistributed in a manner which is experimentally determined to be correlated to the degree of the influence.
- 10 13. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of being redistributed, by modulation of the intracellular pathway, in substantially the same manner as the at least one component of the intracellular pathway.
- 15 14. A method according to any of claims 1-13, wherein the luminophore is a luminophore which is capable of being quenched upon spatial association with a component which is redistributed by modulation of the pathway, the quenching being measured as a decrease in the intensity of the luminescence.
- 20 15. A method according to any of claims 1-13, wherein the variation or result with respect to the spatially distributed light emitted by the luminophore is detected by a change in the resonance energy transfer between the luminophore and another luminescent entity capable of delivering energy to the luminophore, each of which has been selected or engineered to become part of, bound to or associated with particular components of the intracellular pathway, and one of which undergoes redistribution in response to the influence, thereby changing the 25 amount of resonance energy transfer, the change in the resonance energy transfer being measured as a change in the intensity of emission from the luminophore.
- 30 16. A method according to claim 15, wherein the change in the intensity of the emission from the luminophore is sensed by a single channel photodetector which responds only to the average intensity of the luminophore in a non-spatially resolved fashion

17. A method according to any of claims 1-16, wherein the property of the light being recorded is intensity, fluorescence lifetime, polarization, wavelength shift, or other property which is modulated as a result of the underlying cellular response.

5

18. A method according to any of claims 1-15 or 17, wherein the recording of the spatially distributed light is performed using a recording system which records the spatial distribution of a recordable property of the light in the form of an ordered array of values.

10 19. A method according to claim 18, wherein the recording of the spatial distribution of the recordable property of the light is performed using a charge transfer device such as a CCD array or a vacuum tube device such as a vidicon tube.

15 20. A method according to any of the preceding claims, wherein the light to be measured passes through a filter which selects the desired component of the light to be measured and rejects other components.

21. A method according to any of the preceding claims, wherein the recording of the spatial distribution of the recordable property of light is performed by fluorescence microscopy.

20

22. A method according to any of the preceding claims, wherein the recording of the variation or result with respect to light emitted from the luminophore is performed by recording the spatially distributed light as one or more digital images, and the processing of the recorded variation to reduce it to one or more numbers representative of the degree of redistribution
25 comprises a digital image processing procedure or combination of digital image processing procedures.

23. A method according to any of claims 2-22, wherein the intracellular pathway is an intra-cellular signalling pathway.

24. A method according to any of the preceding claims, wherein the luminophore is a fluorophore.
- 5 25. A method according to any of the preceding claims wherein the luminophore is a polypeptide encoded by and expressed from a nucleotide sequence harboured in the cell or cells.
- 10 26. A method according to any of the preceding claims, wherein the luminophore is a hybrid polypeptide comprising a fusion of at least a portion of each of two polypeptides one of which comprises a luminescent polypeptide and the other one of which comprises a biologically active polypeptide, as defined herein.
- 15 27. A method according to claim 26, wherein the luminescent polypeptide is a GFP as defined herein.
- 20 28. A method according to claim 27 wherein the GFP is selected from the group consisting of green fluorescent proteins having the F64L mutation as defined herein.
- 25 29. A method according to claim 28 wherein the GFP is a GFP variant selected from the group consisting of F64L-GFP, F64L-Y66H-GFP, F64L-S65T-GFP, and EGFP.
30. A method according to any of the previous claims for detecting intracellular translocation of a biologically active polypeptide affecting intracellular processes upon activation, the
method comprising
- a) culturing one or more cells containing a nucleotide sequence coding for a hybrid polypeptide comprising a GFP which is N- or C-terminally tagged, optionally through a linker, to a biologically active polypeptide under conditions permitting expression of the nucleotide sequence,

306

- 5 b) modulating the activity of the biologically active polypeptide by incubating the cell or cells with a substance having biological activity and
c) measuring the fluorescence produced by the incubated cell or cells and determining the result or variation with respect to the fluorescence, such result or variation being indicative of the translocation of a biologically active polypeptide in said cell.

31. A method according to claim 30, wherein the nucleotide sequence is a DNA sequence.

32. A method according to claim 30 or 31, wherein the modulation is an activation.

10

33. A method according to claim 30 or 31, wherein the modulation is a deactivation.

15

34. A method according to any of claims 30-33 wherein the fluorescence of the cell or cells is measured prior to the modulation, and the result or variation determined in step (c) is a change in fluorescence compared to the fluorescence measured prior to the modulation.

35. A method according to any of claims 30-34, wherein the intracellular processes are intracellular signalling pathways.

20

36. A method according to claim 34, wherein the change in fluorescence measured in step (c) comprises determining a change in the spatial distribution of the fluorescence.

25

37. A method according to any of the preceding claims wherein the mechanically intact living cell or cells is/are a mammalian cell/mammalian cells which, during the time period over which the influence is observed, is/are incubated at a temperature of 30°C or above, preferably at a temperature of from 32°C to 39°C, more preferably at a temperature of from 35°C to 38°C, and most preferably at a temperature of about 37°C.

38. A method according to any of the preceding claims, wherein the at least one mechanically intact living cell is part of a matrix of identical or non-identical cells.
39. A method according to any of claims 1-36 and 38, wherein the cell or cells is/are selected from the group consisting of fungal cells, such as a yeast cell; invertebrate cells including insect cells; and vertebrate cells, such as mammalian cells.
40. A nucleic acid construct coding for a fusion polypeptide comprising a biologically active polypeptide that is a component of an intracellular signalling pathway, or a part thereof, and a GFP, with the proviso that the construct is not a construct coding for a fusion polypeptide in which the biologically active polypeptide is selected from the group consisting of PKC-alpha, PKC-gamma, and PKC-epsilon.
41. A nucleic acid construct coding for a fusion polypeptide comprising a biologically active polypeptide that is a component of an intracellular signalling pathway, or a part thereof, and an F64L mutant of GFP.
42. A nucleic acid construct according to claim 40 or 41, wherein the biologically active polypeptide is a protein kinase or a phosphatase.
43. A nucleic acid construct according to any of claims 40-42 wherein the GFP is N- or C-terminally tagged, optionally via a peptide linker, to the biologically active polypeptide or part thereof.
44. A nucleic acid construct according to any of claims 40, 41 and 43, wherein the biologically active polypeptide is a transcription factor or a part thereof which changes cellular localisation upon activation.

45. A nucleic acid construct according to any of claims 40, 41 and 43, wherein the biologically active polypeptide is a protein, or a part thereof, which is associated with the cytoskeletal network and which changes cellular localisation upon activation.
- 5 46. A nucleic acid construct according to any of claims 40-43, wherein the biologically active polypeptide is a protein kinase or a part thereof which changes cellular localisation upon activation.
- 10 47. A nucleic acid construct according to claim 46, wherein the protein kinase is a serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.
- 15 48. A nucleic acid construct according to claim 46, wherein the protein kinase is a tyrosine protein kinase or a part thereof capable of changing intracellular localisation upon activation.
- 19 49. A nucleic acid construct according to claim 46, wherein the protein kinase is a phospholipid-dependent serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.
- 20 50. A nucleic acid construct according to claim 46, wherein the protein kinase is a cAMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation.
- 25 51. A nucleic acid construct according to claim 50 which codes for a PKAc-F64L-S65T-GFP fusion.
- 29 52. A nucleic acid construct according to claim 46, wherein the protein kinase is a cGMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation.

53. A nucleic acid construct according to claim 46, wherein the protein kinase is a calmodulin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

5

54. A nucleic acid construct according to claim 46, wherein the protein kinase is a mitogen-activated serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

10 55. A nucleic acid construct according to claim 54, which codes for an ERK1-F64L-S65T-GFP fusion.

56. A nucleic acid construct according to claim 54, which codes for an EGFP-ERK1 fusion.

15 57. A nucleic acid construct according to claim 46, wherein the protein kinase is a cyclin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

20 58. A nucleic acid construct according to claim 42 or 43, wherein the biologically active polypeptide is a protein phosphatase or a part thereof capable of changing cellular localisation upon activation.

59. A nucleic acid construct according to any of claims 40-58 which is a DNA construct.

25 60. A nucleic acid construct according to any of claims 40-59 wherein the gene encoding GFP is derived from *Aequorea victoria*.

61. A nucleic acid construct according to claim 60 in which the gene encoding GFP is the gene encoding EGFP as defined herein.

62. A nucleic acid construct according to claim 60 in which the gene encoding a GFP is a gene encoding a GFP variant selected from F64L-GFP, F64L-Y66H-GFP and F64L-S65T-GFP.

5

63. A DNA construct according to claim 59 and 61 or, where applicable, 62, which is a construct as identified by any of the DNA sequences shown in SEQ ID NO: 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, and 142, or is a variant thereof capable of encoding the same fusion polypeptide or a fusion polypeptide which is biologically equivalent thereto, as defined herein.

10 64. A cell containing a nucleic acid construct according to any of claims 40-63 and capable of expressing the sequence encoded by the construct.

15

65. A cell according to claim 64, which is a eukaryotic cell.

20

66. A cell according to claim 64, which is selected from the group consisting of fungal cells, such as yeast cells; invertebrate cells, including insect cells, and vertebrate cells, such as mammalian cells.

67. A cell according to claim 66, which is a mammalian cell.

25

68. An organism carrying in at least one of its component cells a nucleic acid sequence as contained in the constructs according to any of claims 40-59, said cell being capable of expressing said nucleic acid sequence.

69. An organism according to claim 68 which is selected from the group consisting of unicellular and multicellular organisms, such as a mammal.

70. A fluorescent probe comprising a GFP which is N- or C-terminally tagged, optionally via a peptide linker, to a biologically active polypeptide or a part or a subunit thereof which is a component of an intracellular signalling pathway as defined herein, the probe being a probe
5 which is encoded by the nucleic acid construct according to any of claims 40-59.
71. A method according to any of claims 1-39, wherein the luminophore is a fusion polypeptide as encoded by the nucleic acid construct according to any of claims 40-63.
- 10 72. A method according to any of claims 1-39 or 71 in which the method of the invention is used in a screening program as defined herein.
73. An apparatus for measuring the distribution of fluorescence in at least one cell, and thereby any change in the distribution of fluorescence in at least one cell, which includes the
15 following component parts: (a) a light source, (b) a means for selecting the wavelength(s) of light from the source which will excite the fluorescence of the protein, (c) a means for rapidly blocking or passing the excitation light into the rest of the system, (d) a series of optical elements for conveying the excitation light to the specimen, collecting the emitted fluorescence in a spatially resolved fashion, and forming an image from this fluorescence, (e) a
20 bench or stand which holds the container of the cells being measured in a predetermined geometry with respect to the series of optical elements, (f) a detector to record the spatially resolved fluorescence in the form of an image, (g) a computer or electronic system and associated software to acquire and store the recorded images, and to compute the degree of redistribution from the recorded images.
- 25
74. An apparatus according to claim 73 in which some or all of the system is automated.
75. An apparatus according to claim 73 in which components d and e comprise a fluorescence microscope.

312

76. An apparatus according to claim 73 in which component f is a CCD camera.

77. An apparatus according to claim 73 in which the image is formed and recorded by an optical scanning system.

5

78. An apparatus according to claim 73 in which a liquid addition system is used to add a known or unknown compound to any or all of the cells in the cell holder at a time determined in advance.

10 79. An apparatus according to claim 78 in which the liquid addition system is under the control of the computer or electronic system.

15 80. A method according to any of claims 1-79 wherein the method is a screening program for the identification of a biologically active substance as defined herein that directly or indirectly affects an intracellular signalling pathway and is potentially useful as a medicament, wherein the result of the individual measurement of each substance being screened which indicates its potential biological activity is based on measurement of the redistribution of spatially resolved luminescence in living cells and which undergoes a change in distribution upon activation of an intracellular signalling pathway.

20

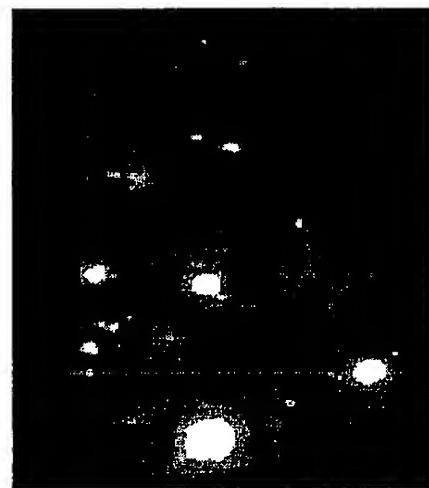
81 A method according to any of claims 1-79 wherein the method is a screening program for the identification of a biologically toxic substance as defined herein that exerts its toxic effect by interfering with an intracellular signalling pathway, wherein the result of the individual measurement of each substance being screened which indicates its potential biologically toxic activity is based on measurement of the redistribution of said fluorescent probe in living cells and which undergoes a change in distribution upon activation of an intracellular signalling pathway.

30 82. A method according to any of claims 1-80 wherein a fluorescent probe is used in back-tracking of signal transduction pathways as defined herein.

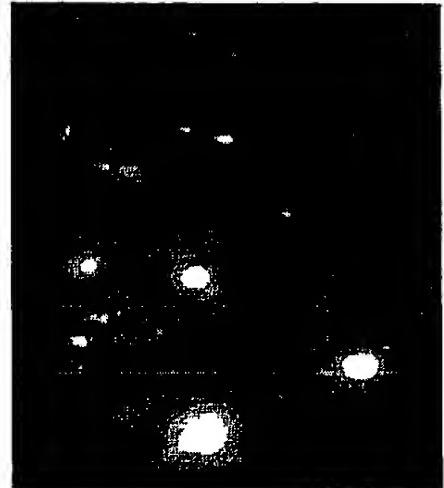
83. A method of treating a condition or disease related to the intracellular function of a protein kinase comprising administering to a patient suffering from said condition or disease an effective amount of a compound which has been discovered by any method according to the
5 invention.
84. A compound that modulates a component of an intracellular pathway as defined herein, as determined by a method according to the method of the invention.
- 10 85. A medical composition comprising a therapeutic amount of a compound identified according the method of the invention.
- 15 86. A method of selectively treating a patient suffering from an ailment which responds to medical treatment comprising obtaining a primary cell or cells from said patient, transfecting the cell or cells with at least one DNA sequence encoding a fluorescent probe according to the invention, culturing the cell or cells under conditions permitting the expression of said probes and exposing it to an array of medicaments suspected of being capable of alleviating said ailment, then comparing changes in fluorescence patterns or redistribution patterns of the fluorescent probes in the intact living cell or cells to detect the cellular response to the
20 specific medicaments (obtaining a cellular action profile), then selecting a medicament(s) based on desired activity and acceptable level of side effects and administering an effective amount of said medicament(s) to said patient.
- 25 87. A method according to any of claims 1-80 of identifying a drug target among the group of biologically active polypeptides which are components of intracellular signalling pathways.

1 / 12

Fig 1



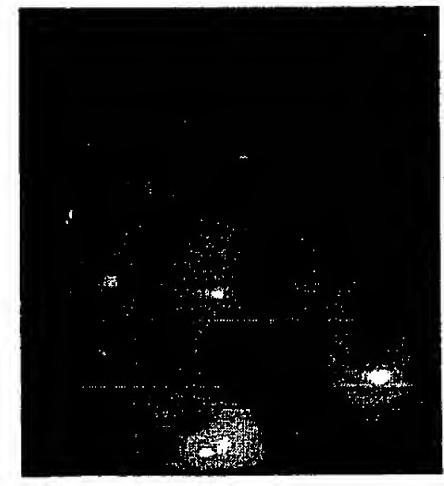
a)



b)



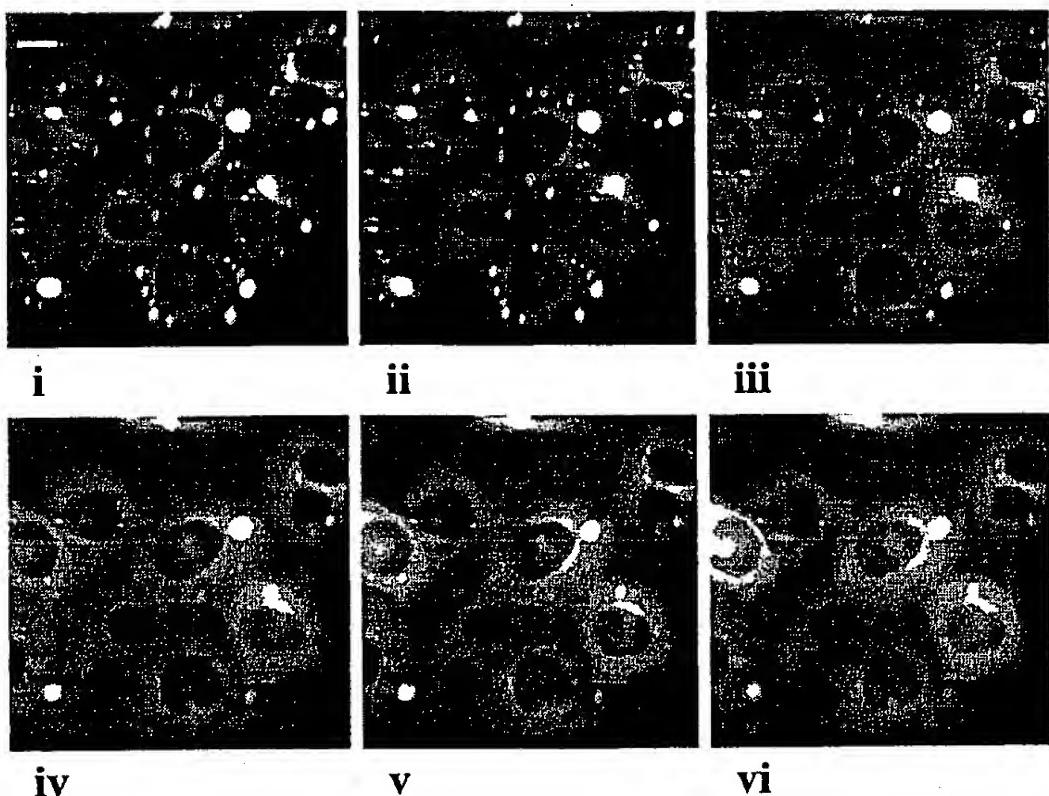
c)



d)

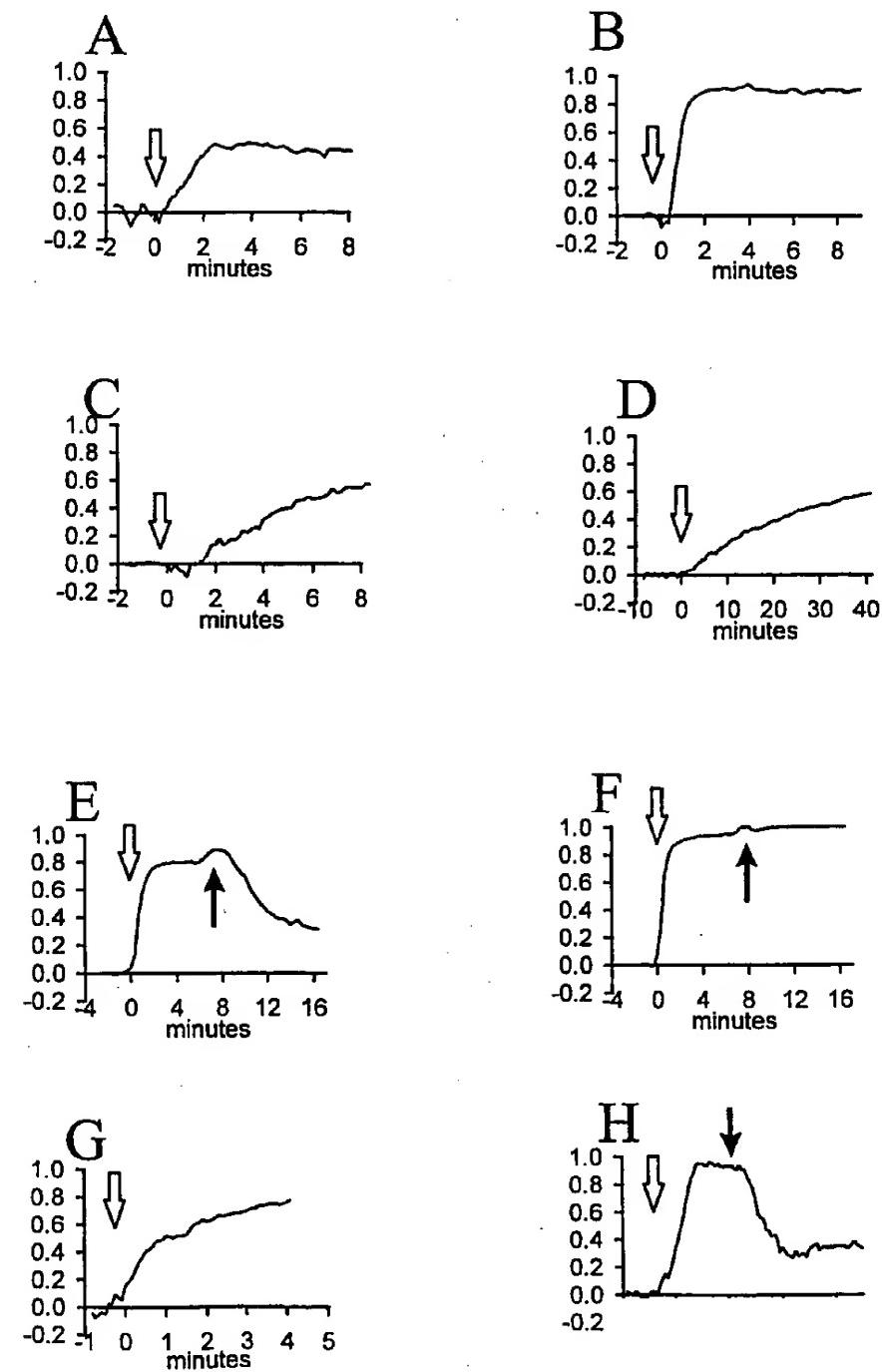
2/12

Fig 2



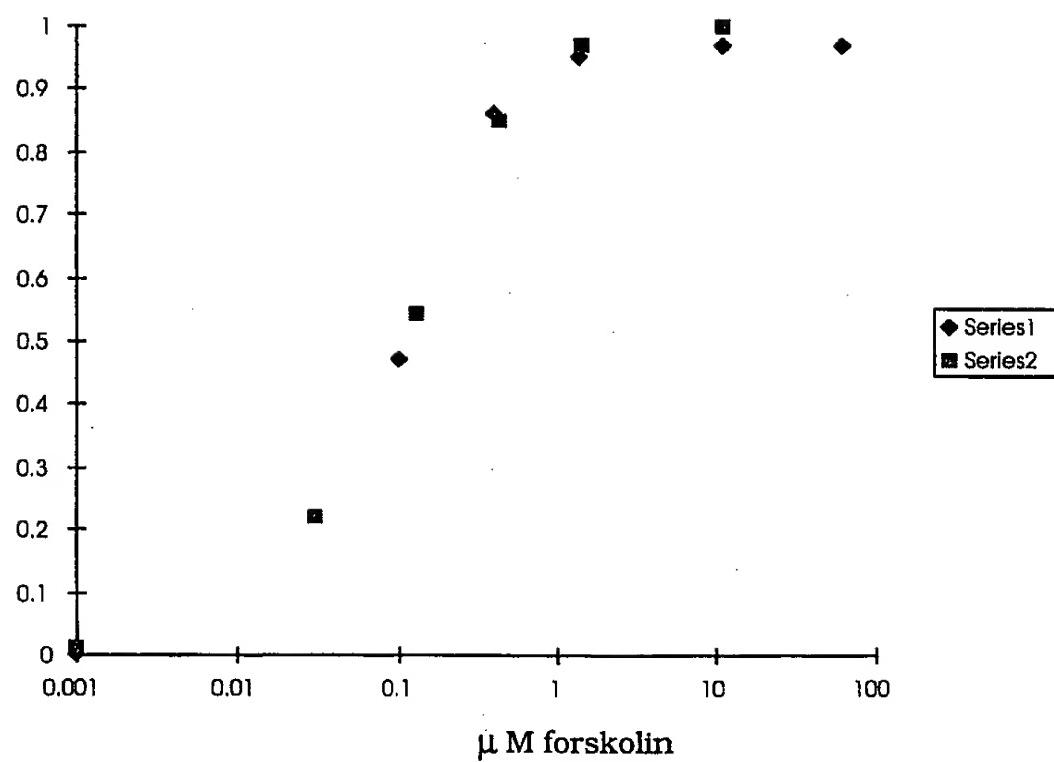
3 / 12

Fig 3



4/12

Fig 4



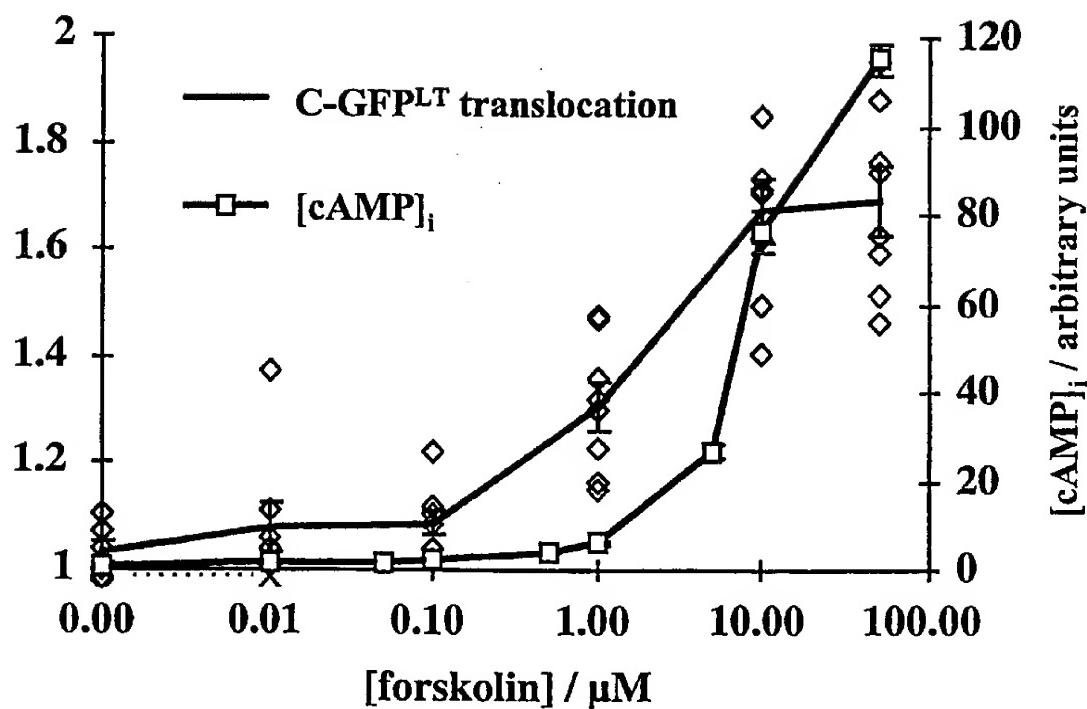
5 / 12

Fig 5

[forskolin] μ M	$t_{1/2\max}$ / s	t_{\max} / s
1	115±21	310±31
10	69±14	224±47
50	47±10	125±28

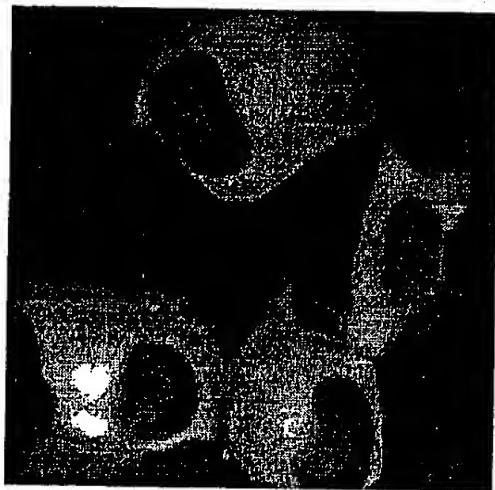
6 / 12

Fig 6



7 /12

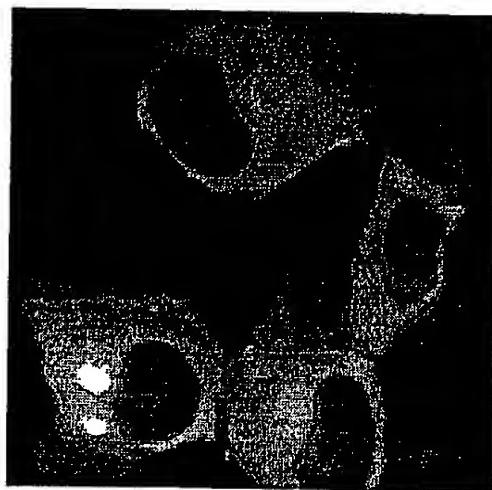
Fig 7



a)



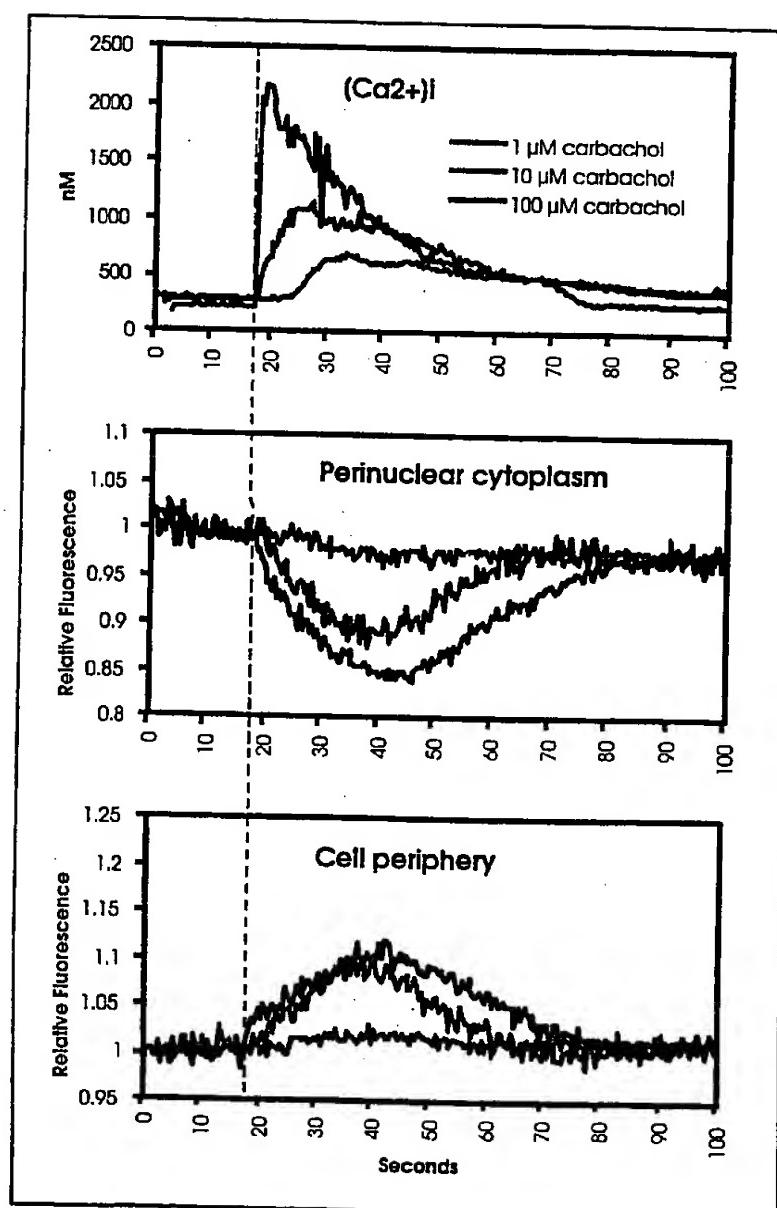
b)



c)

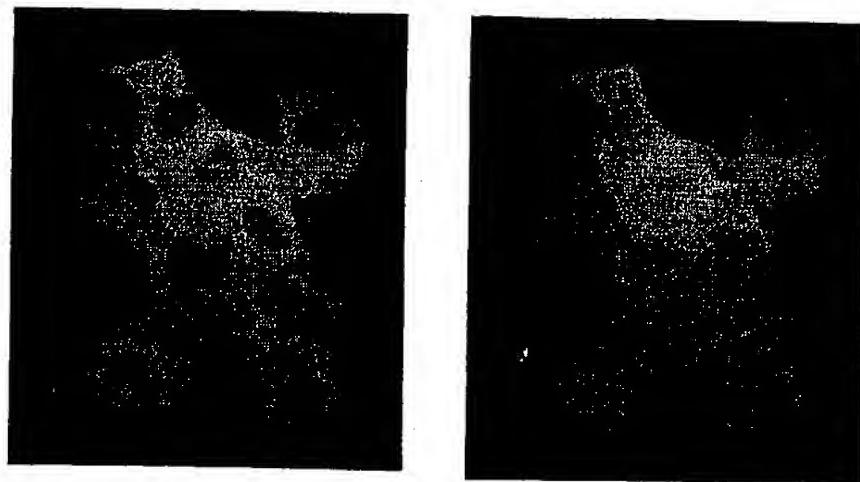
8 /12

Fig 8



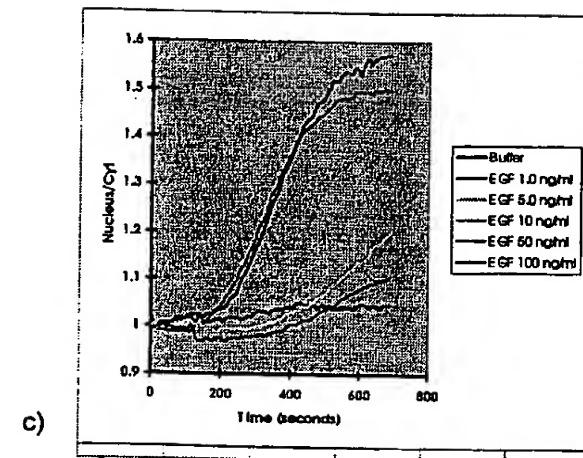
9 / 12

Fig 9

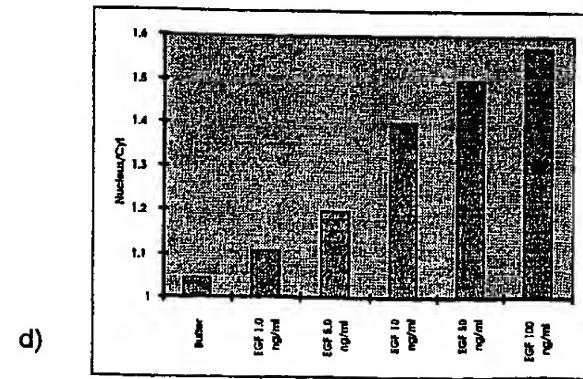


a)

b)

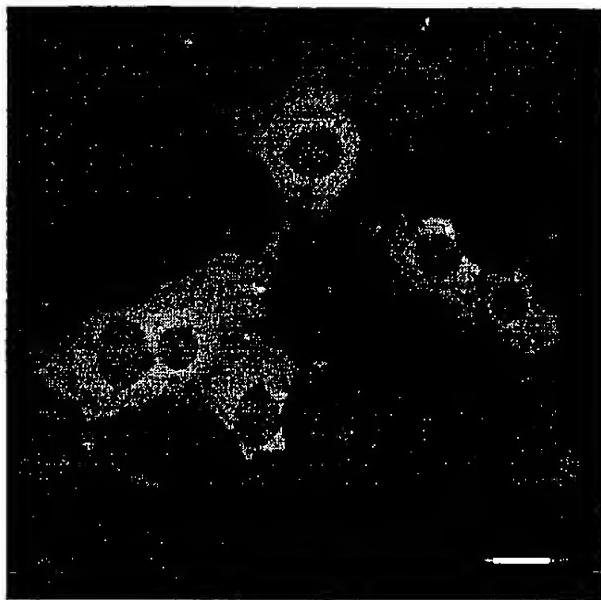
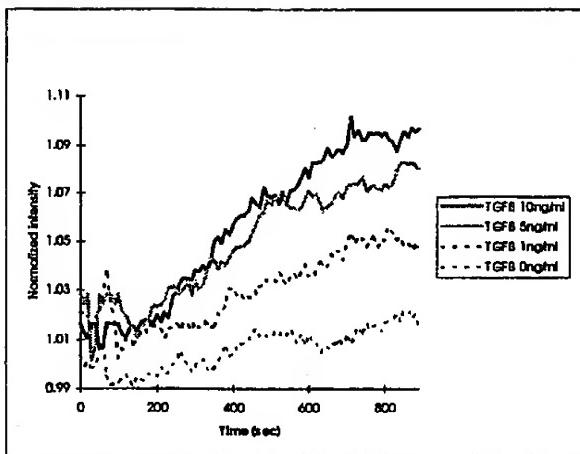
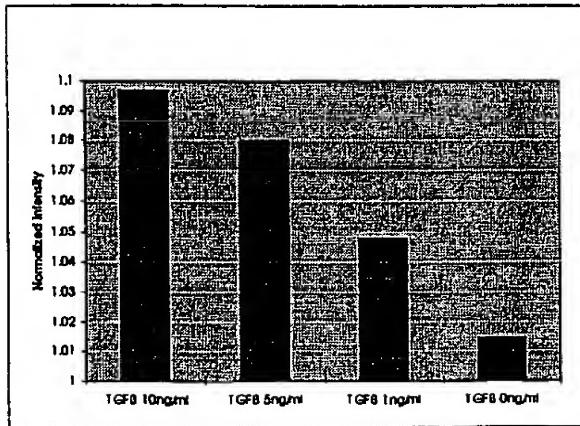


c)



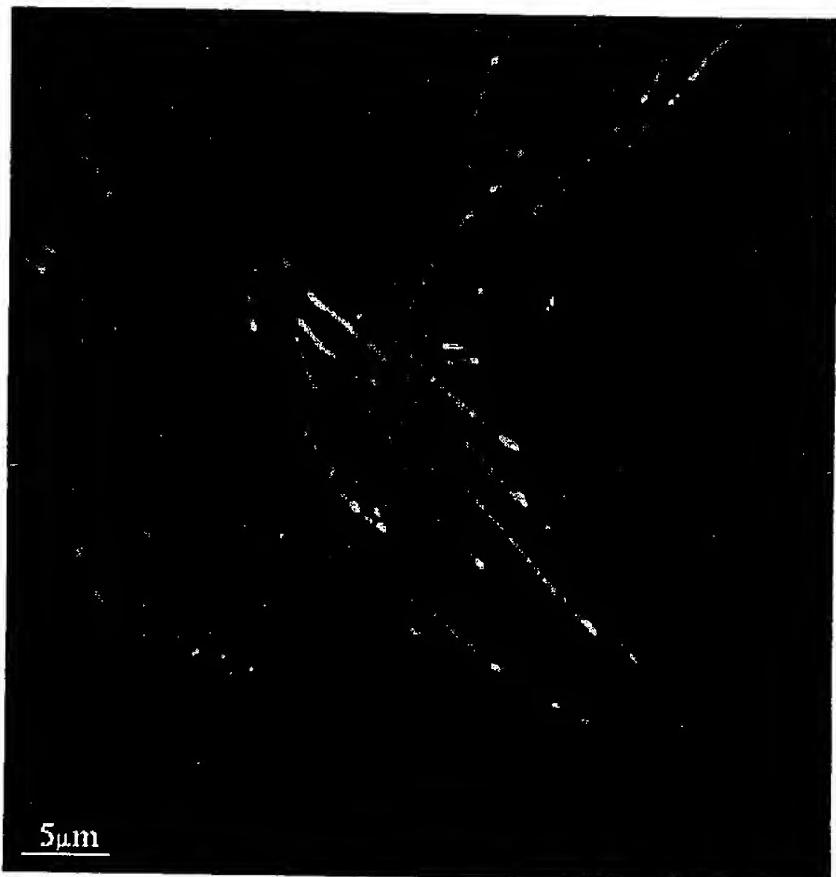
d)

10 /12

Fig 10**a)****b)****c)**

11/12

Fig 11



12 / 12

Fig. 12

